

## **FIGURE 1**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGCTGGTAAGGATTACAAAGGTGCAGGTATG  
AGCAGGTCTGAAGACTAACATTGTGAAGTTGTAACAGAAAACAGAAATGTGGTGGT  
TTCAGCAAGGCCTCAGTTCCCTTCAGCCCTTGTAAATTGGACATCTGCTGCTTCATATT  
TCATAACATTACTGCAGTAACACTCCACCATAAGACCCGGCTTACCTTATATCAGTGACACTGG  
TACAGTAGCTCCAGAAAAATGCTTATTGGGCAATGCTAAATATTGCGGCAGTTTATGCATTG  
CTACCATTTATGTTGTTAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAA  
TTAAACAAGGCTGGCCTTGTACTTGAATACTGAGTTGTTAGGACTTCTATTGTGGCAAACCTT  
CCAGAAAAACAACCCCTTTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTGGTATGGCCTCAT  
TATATATGTTGTTCAGACCATCCTTCTACCAAATGCAGCCAAATCCATGGCAAACAGTC  
TTCTGGATCAGACTGTTGGTTATCTGGTGTGGAGTAAGTGCACTTAGCATGCTGACTGCTC  
ATCAGTTTGACAGTGGCAATTGGACTGATTAGAACAGAAACTCCATTGGAACCCGGAGG  
ACAAAGGTTATGTGCTCACATGATCACTACTGCAGCAGAATGGTATGTCTTCTTCTT  
GGTTTTCTGACTTACATTGTGATTTCAAGAAAATTCTTACGGGTGGAAGCCAATTACA  
TGGATTAACCCCTATGACACTGCACCTGCCCTATTAAACATGAACGAACACGGCTACTTCCA  
GAGATATTTGATGAAAGGATAAAAATTCTGTAATGATTGATTCTCAGGGATTGGGGAAAGG  
TTCACAGAAGTTGCTTATTCTCTGAAATTCAACCACTTAATCAAGGCTGACAGTAACACT  
GATGAATGCTGATAATCAGGAAACATGAAAGAACGCCATTGATAGATTATTCTAAAGGATATCAT  
CAAGAACACTATTAAAACACCTATGCCTATACCTTTATCTCAGAAAATAAGTCAAAAGACT  
ATG

## **FIGURE 2**

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV  
LCIATIYVRYKQVHALSPEENVIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG  
MGSLYMFVQTILSYQMOPKIHGKQVFIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW  
NPEDKGYVLHMITTAEWSMSFSFFGFFLTYIRDQKISLRVEANLHGLTLYDTAPCPINNERTR  
LLSRDI

**Important features:**

**Type II transmembrane domain:**

amino acids 13-33

**Other Transmembrane domains:**

amino acids 54-73, 94-113, 160-180, 122-141

**N-myristoylation sites.**

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

### **FIGURE 3**

CGGACGCGTGGCGGACCGTGGGGAGAGCCGCAGTCGGCTGCAGCACCTGGAGAAGGCAGACC  
GTGTGAGGGGGCCTGGCCCCAGCGTGTGGCTCGGGAGTGGAAAGTGGAGGCAGGAGCCITC  
CTTACACTTCGCCTGAGTTCCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTG  
GATTTGGGTGGCTTTCTTCATGCGCCAATTGTTAAAGACTATGAGATACGTCAGTATGTTGACAG  
GTGATCTCTCGTGACGTTGCATTTCTTGACCATGTTGAGCTCATCATCTTGAAATCTTAGG  
AGTATTGAATAGCAGCTCCCGTATTCACTGGAAAATGAACCTGTGTGAATTCTGCTGATCCTGG  
TTTCATGGTGCCTTTTACATGGCTATTTATTGTGAGCAATATCCGACTACTGCATAAACACGA  
CTGCTTTTTCTGTCTTATGGCTGACCTTATGTATTCTCTGGAAACTAGGAGATCCCTTCC  
CATTCTCAGCCCCAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAG  
TGACTCTCATGGCTCTCTGGATTGGTGTCAACTGCCATACACTACATGTCTTACTTC  
CTCAGGAATGTGACTGACACGGATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT  
CATAAAGAAAAAGAAAAGGATGGCAATGGCACGGAGAACAAATGTTCCAGAAGGGGAAGTGCATAACA  
AACCATCAGGTTCTGGGAATGATAAAAAGTGTACCACTTCAGCATCAGGAAGTGAATCTTACT  
CTTATTCAACAGGAAGTGGATGCTTGGAAAGATTAAGCAGGCAGCTTCTGGAAACAGCTGATCT  
ATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTCAAGGGAAATATTTAATTTCTTGGTT  
ACTTTTCTCTATTTACTGTGTTGGAAAATTCATGGCTACCATCAATATTGTTTGATCGAGTT  
GGGAAAACGGATCCTGTACAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTGATGT  
GAAGTTTGGTCCAACACATTCTCATCTTGTGGAATAATCGTCACATCCATCAGAGGAT  
TGCTGATCACTCTTACCAAGTTCTTATGCCATCTCTAGCAGTAAGTCTCCAATGTCATTGCTCTG  
CTATTAGCACAGATAATGGCATGTACTTGTCTCCTCTGTGCTGATCGAATGAGTATGCCTT  
AGAATACCGCACCATAATCACTGAAGTCTGGAGAACTGCAGTTCAACTCTATCACCGTTGGTTG  
ATGTGATCTCCTGGTCAGCGCTCTCTAGCATACTCTCTATGGCTCACAAACAGGCACCA  
GAGAACAAATGGCACTTGACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTCAAATTAA  
GATATAAGAGGGGGAAAAATGGAACCAGGGCTGACATTATAAACAAACAAAATGCTATGGTAGC  
ATTTTCACCTTCATAGCATACTCTTCCCGTCAGGTGATACTATGACCATGAGTAGCATCAGCCAG  
AACATGAGAGGGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCGTGTGGATATGAGGCTGG  
TGTAGAGGCGGAGAGGAGCCAAGAAACTAAAGGTGAAAATACACTGGAACCTGGGGCAAGACATGT  
CTATGGTAGCTGAGCCAAACACGTAGGATTCCGTTAAGGTTACATGGAAAGGTTATAGCTTG  
CCTTGAGATTGACTCATTAACACAGAGACTGTAACAAAAAAAAAAAAAGGGCGGCCGCG  
ACTCTAGAGTCGACCTGCAGAAGCTGGCCGCCATGGCCAACCTGTTATTGCAGCTTATAATG

## **FIGURE 4**

MSFLIDSSIMITSQILFFFGFWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGV  
LNSSSRYFHWKMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTMYFFWKLGD  
FPILSPKKGILSIEQLISRVGIVGVTLMALLSGFGAVNCPTYMSYFLRNVTDTDILALERLLQ  
TMDMIISKKKRMAMARRTMFQKGEVHNKPSPGFWMKSVTTTSASGESENLTLIQQEVDALEELSRO  
LFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVGKTDPVTRGIEI  
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLAQMIMGMY  
FVSSVLLIRMSMPLERYTIIITEVLGELQFMFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

**Important features:**

**Signal peptide:**

amino acids 1-23

**Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

**Eukaryotic cobalamin-binding proteins**

amino acids 151-160

## **FIGURE 5**

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGAGGCCAACATAGTTCC  
AGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCACTGGCCATCTGAGGTT  
GTTTCCCCTGGCTCTGAAGGGGTAGGCACCATGGCCAGGTGCTCAGGCTGGTGTGCTCTCACT  
TCCATCTGGACCACGAGGCTCTGGTCAAGGCTTTGCGTGCAGAAGAGCTTCCATCCAGGT  
GTCATGCAGAATTATGGGGATCACCCCTGAGCAAAAAGGCGAACAGCAGCTGAATTTCACAG  
AAGCTAAGGAGGCCTGAGGCTGCTGGACTAAGTTGCCGGCAAGGACCAAGTGAACAGCC  
TTGAAAGCTAGCTTGAACACTTCAGCTATGGCTGGGTTGGAGATGGATTGTTGCTACTCTAG  
GATTAGCCCCAACCCCAAGTGTGGAAAAATGGGGTGGGTGCTGTATTGAAAGGTTCCAGTG  
GCCGACAGTTGAGCCTATTGTTACAACCTATCTGATACTTGGACTAACCTCGCATTCCAGAA  
ATTATCACCACCAAAGATCCCATTCAACACTCAAACCTGCAACACAAACAGAATTATTATGT  
CAGTGACAGTACCTACTCGGTGGCATCCCTTAECTCTACAATACCTGCCCTACTACTACTCC  
CTGCTCCAGCTCCACTCTATTCCACGGAGAAAAAATTGATTGTCACAGAAGTTTATG  
GAAACTAGCACCAGTCTACAGAAACTGAACCATTGTTGAAAGTAAAGCAGCATCAAGAATGA  
AGCTGCTGGTTTGAGGTGCCCCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTG  
CAGCTGGCTTGGATTGCTATGTCAAAAGGTATGTGAAGGCTTCCCTTACAACAAAGAAT  
CAGCAGAAGGAAATGATCGAAACCAAAAGTAGTAAAGGAGGAGAAGGCCATGATAGCAACCTAA  
TGAGGAATCAAAGAAACTGATAAAAACCCAGAACAGAGTCCAAGAGTCCAAGC  
GATGCCCTGGAAGCTGAAGT TTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTT  
CATGCTCCTAACCTGCCCCAGCTGGGAAATCAAAGGGCAAAAGAACCAAAGAACAAAGTCCA  
CCCTGGTCTTAACTGGAATCAGCTCAGGACTGCGATTTGACTATGGAGTGCACCAAAGAAT  
GCCCTTCTCTTATTGTAACCCGTCTGGATCTTCTACCTCCAAAGCTCCACGGCCT  
TTCTAGCCCTGGCTATGCTCTAATAATCTTCACTGGGAGAAAGGAGTTTGCAAGTGCAAGGAC  
CTAAAAACATCTCATCAGTATCCAGTGGTAAAGGCCCTCTGGCTGCTGAGGCTAGGTGGTTG  
AAAGCCAAGGAGTCAGTGGAGACCAAGGCTTCTCTACTGATTCCGAGCTCAGGCCCTTCTTCA  
GCTCTGAAGAGAACACGTATCCACCTGACATGCTTCTGGAGCCGGTAAGACCAAAAGAAT  
GGCAGAAAAGTTAGGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTGTAAA  
GCTAAAATAAAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGTAAC  
ACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGAATCAGTTAGAACACACACA  
CTTACTTTTCTGGCTCTACCACTGCTGATATTCTCTAGGAAATATACTTTACAAGTAACA  
AAAATAAAACTCTATAAAATTCTATTCTGAGTTACAGAAATGATTACTAAGGAAGATT  
ACTCAGTAATTGTTAAAAGTAATAAAATTCAACAAACATTGCTGAATAGCTACTATAATGTC  
AAAGTGCTGCAAGGTTTACACTCTGTAATTGAATATTCTCTCAAAAGTGCACATAGTAG  
AACGCTATCTGGGAAGCTATTCTTCTGAGTTGATATTCTAGCTATCTACTTCCAAACATA  
TTTATTCTGCTGAGACTAATCTTATTCTATAATGGCAACCATTATAACCTTAATT  
TATTATTAACATACCTAAGAAGTACATTGTAACCTCTATATACCAAAAGCACATTAAAAGTGCC  
ATTAACAAATGTATCACTAGGCCCTCTTCTCAACAAGAAGGGACTGAGAGATGCAGAAATATT  
TGTGACAAAAAATTAAAGCATTAGAAAATT

## **FIGURE 6**

MARCFSLVLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG  
LSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNCGKNGVGVLIWKPVSRQFAAYCYN  
SSDTWNTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTPPAPASTSIPR  
RKKLICVTEVFMETSTMSTETEPFVENKAASKNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVK  
RYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 7**

CGCCGCGCTCCCGCACCGCGGGCCGCCACCGCGCCGCTCCGCATCTGCACCCGAGCCCGC  
GGCCTCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCACTCGGTCCAGTCGGGC  
CGGCTGGGGCGCAGAGCGGAGATGCAGCGCTGGGCCACCTGCTGTGCCTGCTGGCG  
CGGCGGTCCCCACGGCCCCCGCCGCTCCGACGGCACCTCGGTCCAGTCAGGCCGGCC  
GCTCTCAGCTACCCGCAGGGAGGAGGCCACCCCTCAATGAGATGTTCCCGAGGTTGAGGA  
GGAGGACACGCAGCACAAATTGCGCAGCGCGTGAAGAGATGGAGGAGAAGAAGCTGCTG  
AAGCATCATCAGAAGTGAACCTGGCAACTACCTCCCAGCTATCACAATGAGACCAACACAGAC  
ACGAAGGTTGAAATAATACCACATGTGCACCGAGAAATTCAAAGAATAACCAACACCAGAC  
TGGACAAATGGCTTTCAGAGACAGTTACACATCTGTTGGAGACGAAGAAGGCAGAAGGAGC  
ACGAGTGCATCATCGACGAGGACTGTGGGCCAGCAGTACTGCCAGTTGCCAGTTCCAGTAC  
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGACAGTGATGCTGTGGAGACCA  
GCTGTGTCTGGGGTCATGTGCACCCAAATGGCCACCAGGGCAGCAATGGGACCATCTGTGACA  
ACCAGAGGGACTGCCAGCGGGGCTGTGCTGTGCCTCCAGAGAGGCCTGCTGTCCCTGTG  
ACACCCCTGCCGTGGAGGGCAGCTTGCCATGACCCGCCAGCCGGCTTCTGGACCTCATCAC  
CTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTGTGCCAGTGGCTCCCTGCCAGC  
CCCACAGCCACAGCCTGGTGTATGTGCAAGCCGACCTCGTGGGGAGCCGTGACCAAGATGG  
GAGATCCTGCTGCCAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTCATGGAGGAGGTGCG  
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCCTGGGGAGCCTGGCTG  
CCGCCGCTGCATGTGGAGGGGAAGAGATTTAGATCTGGACCAGGCTGTGGTAGATGTGCAA  
TAGAAATAGCTAATTATTTCCCAGGTGTGCTTTAGGCTGGCTGACCAGGCTTCTCCTA  
CATCTCTCCCAGTAAGTTCCCCTCTGGCTTGACAGCATGAGGTGTTGCATTTGTTCAGCT  
CCCCCAGGCTGTTCCAGGCTTCACAGTCTGGTGTGGAGAGTCAGGCAGGGTAACTGCA  
GGAGCAGTTGCCACCCCTGTCCAGATTATGGCTGCTTGCCTCTACCAGTGGCAGACAGCCG  
TTTGTCTACATGGCTTGAATTGTTGAGGGAGAGATGGAAACAATGTGGAGTCTCCCTC  
TGATTGGTTGGGAAATGTGGAGAGATGGCTTGCAACATCAACCTGGAAAAATG  
CAACAAATGAATTTCCACGCAGTCTTCCATGGCAGGTAAGCTGTGCCTCAGCTG  
AGATGAAATGTTCTGTCACCCTGCATTACATGTGTTATTCATCCAGCAGTGTGCTCAGTCC  
TACCTCTGCCCAGGGCAGCATTCATATCCAAGATCAATCCCTCTCAGCACAGCCTGGG  
AGGGGGCATTGTTCTCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTGCC  
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCATCTGGTGTGACTCTAACGCTCAGTGTCT  
CTCCACTACCCCACACCAGCCTGGTGCCACAAAAGTGTCTCCCCAAAAGGAAGGAGAATGGGAT  
TTTCTGAGGCATGCACATCTGAATTAGGTCAAACTAATTCTCACATCCCTCTAAAGTAAA  
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGAGCCGTCCTCTAACATGAAGACAATG  
ATTGACACTGTCCCTCTTGGCAGTTGCATAGTAACTTGAAGGTATATGACTGAGCGTAGCA  
TACAGGTTAACCTGCAGAAAACAGTACTTAGGAATTGTAGGGCAGGATTATAAATGAAA  
AAAATCACTTAGCAGCAACGTGAAGACAATTATCAACACAGTGGAGAAATCAACCGAGCAGGGC  
TGTGTGAAACATGGTGTAATATGCACTGCAACACTGAACCTACGCCACCTCAAAATGATG  
TTTCAGGTGTCATGGACTGTTGCCACCTGTATTCATCCAGAGTCTTAAAGTTAAGTGCA  
CATGATTGTATAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAACGTGCATTAGAA  
ATCAAGCATAAAACTCAACGTCAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 8**

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL  
RSAVEEMEAEEAAKASSEVNLPPSYHNETNTDTKGNNTIHVHREIHKITNNQTGQMFSE  
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGRMLCTRSECCGDQLCVWGHC  
TKMATRGSGNTICDNQRDCQPGCCAQRGLLFPVCTPLPVEGELCHDPASRLLDLITWELEPDG  
ALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVRQELEDLE  
RSLTEEMALGEPAAAAALLGGEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 9**

CGGACGGTGGCGGACGCGTGGGGCTGTGAGAAAGTCCAATAAATACATCATGCAACCCCAC  
GGCCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCAGGGCTACTCATCAAAG  
GCCTAATCCAACGTTCTGTCTCAATCTGAAATCTATGGGTCTGGGCTCTTCTGGACCCCTT  
AACTGGGTACTGGCCCTGGGCCATGCGTCTCGCTGGAGCCTTGCCTCTTACTGGGCTT  
CCACAAGCCCCAGGACATCCCTACCTTCCCTTAATCTGCCTTCATCCGACACTCCGTTACC  
ACACTGGGTCAATTGGCATTGGAGCCCTCATCCTGACCCCTGTGAGATAGCCGGGTCACTTGT  
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCCTGAGCCCGCTGCATCATGTGCTGTTT  
CAAGTGCTGCCTCTGGTGTCTGGAAAAATTATCAAGTTCCTAAACCGCAATGCATACATCATGA  
TCGCCATCTACGGGAAGAATTCTGTCTCAGCaaaaATGCCTCATGCTACTCATGCGAAC  
ATTGTCAGGGTGGTGTCTGGACAAAGTCACAGACCTGCTGCTGTTCTTGGAGCTGCTGGT  
GGTCGGAGGCCTGGGGCTCTGCTCTCTCTCCGGTCGATCCCAGGGCTGGTAAAG  
ACTTTAAGAGCCCCCACCTCAACTATTACTGGCTGCCATCATGACCTCCATCCTGGGGCTAT  
GTCATCGCCAGCGGCTCTTCAGCGTTTCCGATGTGTGGACAGCCTCTCCTCTGCTTCC  
GGAAGACCTGGAGCGGAACAAACGGCTCCCTGGACCGCCCTACTACATGTCCAAGAGCCTCTAA  
AGATTCTGGCAAGAAGAACGAGGCGCCCCCGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG  
CCCTGATCCAGGACTGCACCCCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGT  
CTCCATTTGTGGTAAAAAAAGGTTTAGGCCAGGCCTGGCTACGCCTGTAATCCAACACT  
TTGAGAGGCTGAGGCCGGGCGGATCACCTGAGTCAGGAGTTGAGACCAGCCTGGCAACATGGTG  
AAACCTCCGTCTCTATTAAAAACAAAAATTAGCCAGAGTGGTGCATGCACCTGTCACTCC  
GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTGAACCCGGAGGCAGAGGTTGCAGTGAGCCGA  
GATCGGCCACTGCACCTCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAA  
AAGATTTTATTAAAGATATTGTAACTC

## **FIGURE 10**

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCSVQGYSSKGLIQRSVFNLQIYGVLGLFWTL  
NWVLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSIAFGALILTLVQIARVIL  
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAKNAFMLLMRN  
IVRVVVLDKVTDLFFFGLLGVGGVGVLSSSSSGRIPGLGKDFKSPHLNYWLPIMTSILGAY  
VIASGFFSVFGMCVDTLFLCFLEDLERNNNGSLDRPYYMSKSLLKILGKKNEAPPDNKKRKK

**Important features:**

**Transmembrane domains:**

amino acids 57-80 (type II), 110-126, 215-231, 254-274

**N-glycosylation sites.**

amino acids 16-20, 27-31, 289-293

**Hypothetical YBR002c family proteins.**

amino acids 276-288

**Ammonium transporters proteins.**

amino acids 204-231

**N-myristoylation sites.**

amino acids 60-66, 78-84

**Amidation site.**

amino acids 306-310

## **FIGURE 11**

CCCCCGCGCCCGGCCGGCGCCGGCGCCGAAGCCGGGAGCCACCGCCATGGGGCCTGCCTGGGAGCCTGC  
TCCCTGCTCAGCTGCGCGTCTGCCTCTGCAGCTCTGCCCTGCATCCTGTGCAGCTGCTGCCCGC  
CAGCCGCAACTCCACCGTGAGCCGCCTCATCTCACGTTCTCCTCTGGGTGCTGGTGTCCA  
TCATTATGCTGAGCCCAGGGCTGGAGAGTCAGCTCTACAAGCTGCCCTGGGTGTTGAGGAGGGGCC  
GGGATCCCCACCGTCTGCAGGGCACATCGACTGTGGCTCCCTGCTGGCTACCGCCTGTCTACCG  
CATGTGCTTCGCCACGGCGCCTCTTCTTCAACCTGCTCATGCTCTGCCTGAGCAGCA  
GCCGGGACCCCGGGCTGCCATCCAGAATGGGTTGGTCTTTAAGTCTGATCCTGGTGGCCTC  
ACCGTGGGTGCCCTTACATCCCTGACGGCTCCCTCACCAACATCTGGTCTACTTCGGCGTGTGG  
CTCCTTCCTCTTCATCCCTCATCCAGCTGGTGTCTCATCGACTTGCCTGACTCCTGGAACCGGGT  
GGCTGGCAAGGCCAGGGACTGGGATTCCCGTGCCTGGTACCCAGGCTCTCTTCACTCTCC  
TTCTACTTGCTGTCGATCGGGCGTGGCGCTGATGTTCATGTAACACTGAGCCAGCGCTGCCA  
CGAGGGCAAGGTCTTCATCAGCTCACCTCACCTCTGTGTCTGCCTGCTGCCATCGCTGTCTGC  
CCAAGGTCCAGGACGCCAGCCAACTCGGGCTGCTGCAGGCCTGGTCACTCACCCCTACACCAGT  
TTTGTCACTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTGCCAACCCAGCT  
GGGCAACGAGACAGTTGTGGCAGGCCCGAGGGCTATGAGACCCAGTGGTGGATGCCCGAGCATTG  
TGGGCCTCATCATCTTCCTCTGTGCACCCCTTCATCAGTCTGCCTCAGACCCAGGCAGGTG  
AACAGCCTGATGCAAGACCCAGGGACTGCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAGT  
GGCAGCCTGTGAGGCCGGCCTTGACAACGAGCAGGACGGCGTCACTACAGTACTCCTTCC  
ACTTCTGCCTGGTGTGGCTCACTGCACGTCACTGATGACGCTACCAACTGGTACAAGCCCGGTGAG  
ACCCGGAAGATGATCAGCACGTGGACCCGCGTGTGGGTGAAGATCTGTGCCAGCTGGCAGGGCTGCT  
CCTCTACCTGTGGACCCCTGGTAGCCCCACTCCTCCTGCCTGCAACCGCAGTCAGCTGGCAGCCTCA  
CAGCCTGCCATCTGGTGCCTCTGCCACCTGGTGCCTCTGGCTCGGTGACGCCAACCTGCCCTC  
CCCACACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCTGCCCTGCCAGCTCCAGGACCTGCCCTGAGCCGGC  
CTTCTAGTCGTAGTGCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCAC  
ACCCACACGGTGGAGGCTGCCCTTCCTCCCCCTCCCTGGTGTGGCTACACTCAGCATCTGGATGAA  
AGGGCTCCCTGTCCCTCAGGCTCCAGGGAGCGGGCTGCTGGAGAGAGCGGGAACTCCCACACAG  
TGGGGCATCCGGCACTGAAGCCCTGGTGTCCCTGGTCACGTCCCCCAGGGACCCCTGCCCTTCC  
GACTTCGTGCCTTACTGAGTCTAAGACTTTCTAATAAACAAAGCCAGTGCCTGAAAAAAA

## **FIGURE 12**

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIIMLSPGVESQL  
YKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFTLLMLCVSSSRDPRAAIQ  
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQVLVLLIDFAHAWNQRWLGAEC  
ECDSRAWYAGLFFFLLFYLLSIAAVALMFMYYTEPSGCHEGKVFIISLNLTFCVCVSIAAVLPKV  
QDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI  
VGLIIIFLLCTLFISLRSSDHROVNLSLMQTEECPPMLDATQQQQQQVAACEGRAFDNEQDGVTYSY  
SFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVWVKICASWAGLLLWTLVAPLLLNRD  
FS

**Signal sequence:**

amino acids 1-20

**Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

## **FIGURE 13**

CGGGCCAGCCTGGGCAGGCCAGGAACCACCCGTTAAGGTGTCTCTTTAGGGATGGTGA  
GGTTGGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAGAACG  
CTCTCACCGGGAGCCAGAGCTCCATGCTCTCGCGCAATATCCATTCCATCAACCCCACACAA  
CTCATGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTCAGGAGGC  
TTTCTGTTGTTGTCACCTTGACCTCTTATTGTAACATTACTGTGGATAATAGAGTTAAATG  
TGAATGGAGGCATTGAGAACACATTAGAGAACGGGTGATGCAGTATGACTACTATTCTTCATAT  
TTTGATATATTCTCTGGCAGTTTCGATTAAAGTGTAAACTTGCAATGCTGCTGAG  
ACTGCGCCATTGGTGGCAATAGCGTTGACAACGGCAGTGACCAGTCCTTTACTAGCAAAG  
TGATCCTTCGAAGCTTCTCAAGGGCTTGGCTATGTGCTGCCATATTCAATTCA  
CTTGCTGGATTGAGACGTGGCTGGATTCAAAGTGTACCTCAAGAACAGCAGAACAGAAA  
CAGACTCCTGATAGTCAGGATGCTCAGAGAGGGCAGCACTTACCTGGTGGCTTGTGATG  
GTCAGTTTATTCCCCCTCTGAATCCGAAGCAGGATCTGAAGAACGTAAGAAAACAGGACAGT  
GAGAAACCACTTAGAACTATGAGTACTACTTTGTTAAATGTGAAAACCCTACAGAAAGTC  
ATCGAGGCCAAAGAGGCAGGCAGTGAGCTCCCTGTCACAGTAAAGTTGAAATGGTACGTC  
CACTGCTGGCTTATTGAACAGCTAAAGATTTATTGTAATACCTCACAAACGTTGTAC  
CATATCCATGCACATTAGTTGCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTCAATTCTCT  
TCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAGAAAGTCTTGTGCTGTATTCTTAATC  
AAAAGACTTAATATATTGAAGTAACACTTTTAGTAAGCAAGATAACCTTTTATTCAATTCA  
AGAATGGAATTTTTGTTCATGTCTCAGATTATTTGTTGTTAACACTCTACATT  
TCCCTGTTTTAACTCATGCACATGTGCTTTGTACAGTTAAAAGTGTAAATAAAATCTG  
ACATGTCATGTGGCTAGTTTATTGTTCTGATTGTTCTGAAATGTTCTAAACTCTTATTGAAATGC  
CTTGCAAAAGGGAGAAAGGAATTGCGAATACATGAAAATGTCACCAGACATTGTTATT  
TTATCATGAAATCATGTTTCTGATTGTTCTGAAATGTTCTAAACTCTTATTGAAATGC  
ACAAAATGACTTAAACCATTCATATCATGTTCTTGCAGCCAATTCAATTAAAATGAA  
CTAAATTAAAAA

## **FIGURE 14**

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF  
VTLLWIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALT  
AVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPOEAEEENRLLIVQDASER  
AALIPGGLSDGQFYSPPESEAGSEEAEKKQDSEKPLLEL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 54-72, 100-118, 130-144, 146-166

**N-myristoylation sites.**

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

## **FIGURE 15**

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTGGGCCCCACCCGCCAGGAAAGACTGAGG  
CCGC GG CCT GCCCCC CGG C TCC CT GCG CC GCG C C TCC CGG C AGA AAG AT GT GCT CC AG  
GGT CCC CT TG CT GCT GCG CT GCT CT GCT ACT GGG CCT TGGG CT TGGG T GCAGGG CT GCC CAT  
CCGG CT GCC AGT GCAG CC ACAG ACAG T CT T CT GCA CT GCCC CC AGGG ACC AC GG T GCC  
CGAG AC GT GCC ACC CG ACAC GT TGGG CT GT AC GT CT T GAGA AC GG CAT ACC AT GCT CG AC GC  
AGGC AGC TT GCG GC CT GCG GGG CT GCG AGC T CT GG AC CT GT CA CGA ACC AG AT GCG CAG CC  
TGCCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTCGACCTGACGGCCAACAGGCTG  
CATGAAATACCAATGAGACCTTCCGTGGCTTGCGGCCCTCGAGCGCCTCTACCTGGAGCTCAAGCTGC  
CCGC AT CC GCC ACAT CCAGC TGGT GCG CCT TCGACAC GCT CGAC CGC CT CCT GGAGCTCAAGCTGC  
AGGACAACAGAGCTGCGGGCACTGCCCCCGCTGCGCCTGCCCGCCTGCTGCTGGACCTCAGC  
CACAA CAGC CT CCT GGG CCT TGGAGGCCGCACTCTGGACACTGCCAACCTGAGGGCGCTGCGGCT  
GGCTGGTCTGGGGCTGCGAGCAGCTGGACGAGGGGCTCTCAGCCGCTTGCGCAACCTCCACGACC  
TGGATGTGTCGCAACCCAGCTGGAGCGAGCTGACCTGTGATCCGAGGCGCTCCGGGGCCTGACG  
CGCCTGCGGCTGGCGGCAACACCCGCAATTGCCAGCTGCCAGGGCCAGGAGCTGGCGGCGCTGGC  
TGCCCTGCGAGGAGCTGGATGTGAGCAACCTAAGCCTGCAAGGCCCTGCTGGGAGCTCTCGGGCC  
TCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGC  
TGGTTGGCCCCCTGGGTGCGCAGGCCACGTCAACTGGCAGCCCTGAGGAGACGCGCTGCCA  
CTTCCCCCGCAAGAACGCTGGCCGCTGCTGGAGCTGACTACGCCGACTTGGCTGCCAG  
CCACCA CACCACAGCCACAGTGGCCACACAGGAGGCCGTTGGCAGGCCACAGCTTGTCT  
TCTAGCTTGGCTCTTACCTGGCTTAGCCCCACAGCGCCGGCACTGAGGCCCCAGGCCGCC  
CACTGCCCAACCGACTGTAGGCCCTGTCCCCCAGGCCAGGACTGCCACCGTCCACCTGCC  
ATGGGGCACATGCCACCTGGGACACGGCACCCATGGCTGCTGTGCCCCGAAGGCTTACG  
GGCCTGTACTGTGAGAGCCAGATGGGGCAGGGACACGGCCAGGCCACACCAGTCACGCC  
GCCACACGGTCCCTGACCCCTGGGATCGAGCCGGTGA G C C C C A C C T C C T G C C G T G G G G C T G C  
AGCGCTACCTCCAGGGGAGCTCCGTGCA G C T C A G G A G C T C C G T C T C A C C T A T G C A A C C T A T G C  
GGCCCTGATAAGCGCTGGTGA CG CTGCCACTGCCCTGCTCGCTGAGTACACGGTCACCCA  
GCTGCCGCCAACGCCACTTACTCCGTCTGTCA TGCTTTGGGCCGGGGGTGCCGGAGG  
GCGAGGAGGCCCTGCCGGAGGCCATACACCCAGCCGCTCCATGCGCCGCCCTGCCGGTGTCTGGCG  
CAGGCCCGAGGGCAACCTGCCCTCCATGCGCCGCCCTGCCGGTGTCTGGCG  
GCTGGCTGCCGTGGGGCAGCTACTGTGTGCGGGGGGGCATGGCAGCAGCGGCTCAGG  
ACAAAGGGCAGGTGGGGCAGGGCTGGGA C T G G A C T G G A G G G A G T G A A G G T C C C T T G G A G  
CCAGGCCGAAGGAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGTCTGAGTGTGAGGTGCC  
ACTCATGGGCTTCCAGGGCTGGCTCCAGTCACCCCTCCACGCAAAGGCCACATCTAAGGCC  
GAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGA G A G T G G C A G G C C C T C C T G C T G C  
ACACCACGTAAGTTCTCAGCTCCAAACCTCGGGGATGTGTGCA G A C A G G G C T G T G A C C A C A G C T  
GGGCCCTGTTCCCTCTGGACCTCGGTCTCCATCTGTGAGATGCTGTGCCCCAGCTGACGAGCC  
CTAACGTCCCCAGAACCGAGTCCTATGAGGACAGTGTCCGCCCTGCCAAGCTGCAAGTC  
CCTGGGCA CGGCCGGCCCTGCCATGTGCTGGTAACGCA TGCCCTGGCTCTGGCTCTCCAC  
TCCAGGCCGCCCTGGGGCCAGTGAAGGAAGCTCCCCGAAAGAGCAGAGGGAGAGCGGGTAGGC  
GGCTGTGTACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAAAATGGAAAGGAAGATGC  
TTTAGGAACATGTTTGTCTTTAAATATATATTATAAGAGATCCTTCCCATTATCT  
GGGAAGATGTTTCAAAACTCAGAGACAAGGACTTGGTTTGTAAAGACAAACGATGATGATGAA  
GGCCTTTGTAAGAAAAAATAAAGATGAAGTGTGAA

## **FIGURE 16**

MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGIT  
MLDAGSFAGLPGLQLLDSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLRRLERLY  
LGKNRIRHIQPGAFDTLDRLLELKLDNEIRALPPLRIPRLLLLLDSHNSLLALEPGIILDtanve  
ALRLAGLGLQQLDEGLFSRRLNLHDLDVSDNQLERVPPVIRGLRGLTRRLLAGNTRIAQLRPEDL  
AGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFCNCVCPLSWFGPWVRESHVTLASPEE  
TRCHFPPKNAAGRLLLELDYADFGCPATTTATVPTTRPVREPTALSSSLAPTWLSPTAPATEAP  
SPPSTAPPTVGPVPQPDCCPSTCLNGGTCHLGTRHHACLCPEGFTGLYCESQMGQGTRPSPTP  
VTPRPPRSLTGLIEPVSPSTSLRVGLQRYLQGSSVQLRSRLTYRNLSGPDKRIVTLRLPASIAEY  
TVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAV  
LLAALAAVGAAYCVRRGRAMAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGEALPSGSE  
CEVPLMGMGPGLQSPHLAKPYI

**Important features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 579-599

**EGF-like domain cysteine pattern signature.**

amino acids 430-442

**Leucine zipper pattern.**

amino acids 197-219, 269-291

**N-glycosylation sites.**

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

**Tyrosine kinase phosphorylation sites.**

amino acids 124-131, 337-345

**N-myristoylation sites.**

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,  
594-600, 640-646

### **FIGURE 17**

GCAGCGGGCAGGCCGGTGGCTGAGTCGTGGCAGAGGCGAAGGCACAGCTCATGC  
GGTCCGGATAGGGCTGACGCTGCTGTGCGGTGCTGAGCTTGGCTCGCGTCCTCGG  
ATGAAGAAGGCAGCCAGGATGAATCCTTAGATTCCAAGACTACTTGACATCAGATGAGTCAGTA  
AAGGACCATACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTCTGATTCAAAGAACTGAG  
ATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGGAAAGTGTACAG  
AAGATATCAGCTTCTAGACTCCTAAATCAGAAAACAAGGACTATGAAGAGCCAAGAAAGTA  
CGGAAACCAGCTTGACGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTCCCTTCT  
TTTCCTAGATAAGGAGTATGATGAATGTACATCAGATGGGAGGGAAAGATGGCAGACTGTGGTGTG  
CTACAACCTATGACTACAAAGCAGATGAAAAGTGGGCTTTGTGAAACTGAAGAACAGGCTGCT  
AAGAGACGGCAGATGCGAGAACAGGAAATGATGTATCAAACCTGAAATGAAAATCCTTAATGAAAG  
CAATAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA  
CCAAAGCCCTGGAGAGAGTGTATGCTCTTATTGGTGTGATTACTGCCACAGAAATATCCAG  
GCAGCGAGAGAGATTTGAGAAGCTGACTGAGGAAGGCTCTCCAAAGGGACAGACTGCTCTTGG  
CTTCTGTATGCCCTGGACTTGGTGTAAATTCAAGTCAGGCCAAAGGCTCTGTATATTACAT  
TTGGAGCTTGGGGCAATCTAATAGCCCACATGGTTGGTAAGTAGACTTTAGTGGAAAGG  
AATAATATTAACATCAGAAGAATTGGTTATAGCGGCCACAACCTTTCAGCTTCATGATC  
CAGATTGCTTGTATTAAGACCAAATATTCAAGTGAACCTCCCTCAAATTCTGTAAAGGATAT  
AACACATGGAATCTACATGTAATGAAAGTGGGGAGTCCACAATTTCCTTAAATGATTAG  
TTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAAATGGCTCTTTAAATTCTGTGAGTTG  
GAATTGTCAGAATCATTTCATAGATTATCATAATTAAAAATTTCCTTAGTTTCA  
AAATTGTAATGGCTATAGAAAACAACATGAAATATTACAAATTTGCAACATG  
CCTAAGAATTGTTAAATTCTGGAGTTATTGTCAGAATGACTCCAGAGAGCTACTTCTG  
TTTTTACTTCTGATTGGCTGTCTCCATTATTCTGGTCAATTGCTAGTGACACTGT  
GCCTGCTCCAGTAGTCTCATTTCCATTGGCTAATTGTTACTTTCTTGCTAATTGG  
AAGATTAACCTATTAAATAAAATTATGCTAAGATXXXXXXXXXXXXXXXXXXXX  
XXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXXXA

## **FIGURE 18**

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLDSTTTSDESVKDHTTAGRVVAGQIFLDSEESSEL  
ESSIQEEEDSLKSQEGESVTEDISFLESPNPNENKDYEEPKKVRKPALTAIECTAHGEPCHFPFLFLDK  
EYDECTS DGDREDGRILWCATTYDYKADEKWGFCETEEEAAKRRQMQEAEEMMYQTGMKILNGSNKKSQKR  
EAYRYLQKAASMNHTKALERVSYALLFGDYLPPQNIQAAREMFEKLTEEGSPKGQTALGFLYASGLGVN  
SSQAKALVYYTGFALGGNLIAHMVLVSRL

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 195-199, 217-221, 272-276

**Tyrosine kinase phosphorylation site.**

amino acids 220-228

**N-myristoylation sites.**

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

**Glycosaminoglycan attachment site.**

amino acids 267-271

**Microbodies C-terminal targeting signal.**

amino acids 299-303

**Type II fibronectin collagen-binding domain protein.**

amino acids 127-169

**Fructose-bisphosphate aldolase class-II protein.**

amino acids 101-119

## **FIGURE 19**

AATTCAAGATTTAAGCCCATTCTGCAGTGGAAATTCACTGAACACTAGCAAGAGGACACCATCTTCTT  
GTATTATAACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTGGGTGCTAGG  
CCTCCTAATCCTCTGGTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAGACATCACTG  
ATAAGTACATTTTATCACTGGATGTGACTCGGGCTTGGAAACTTGGCAGCCAGAACCTTGT  
AAAAAGGGATTCATGTAATCGCTGCCTGACTGAATCAGGATCAACAGCTTAAAGGCAGA  
AACCTCAGAGAGACTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG  
CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGTCTGATCAATAATGCTGGTGT  
CCCGGCGTGTGGCTCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA  
CCTGTTGGACTCATCAGTGTGACACTAAATATGCTCCCTTGGTCAAGAAAGCTCAAGGGAGAG  
TTATTAAATGTCTCCAGTGTGAGGTCGCCCCATGACTGGCTGACACTAAAGCTTGGTGTGACGTCTC  
TATGCAGTGGAAAGGTTCAATGACAGCTTAAGACGGGACATGAAAGCTTGGTGTGACGTCTC  
ATGCATTGAACCAGGATTGTTCAAAACAAACTTGGCAGATCCAGTAAAGGTAAATTGAAAAAAAC  
TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAAACATATGGAGAAGGTTACATTGAAAAAA  
AGTCTAGACAAACTGAAAGGCAATAATCCTATGTGAACATGGACCTCTCCGGTAGAGTG  
CATGGACCACGCTCTAACAGTCTTCCCTAACAGACTCATTATGCCGCTGGAAAAGATGCCAAA  
TTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTGCAAGACTTTTATTGTTGAAACAGAAA  
GCAGAGCTGGCTAACCCAAAGGCAGTGTGACTCAGCTAACACAAATGTCTCCTCCAGGCTATGA  
AATTGGCCGATTCAGAACACATCTCCTTTCAACCCATTCTTATCTGCTCCAACCTGGACT  
CATTTAGATCGTCTTGGATTGCAAAAGGGAGTCCACCATCGCTGGTGTATCCAGGGT  
CCCTGCTCAAGTTCTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCT  
GTATTAGGCTTGCCTGCTGGTGTGATGTAAGGAAATTGAAAGACTTGGCCATTCAAAATGA  
TCTTTACCGTGGCCTGCCCATGCTTATGGTCCCAGCATTACAGTAACCTGTGAATGTTAAGT  
ATCATCTCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 20**

MLFWVLGLLILCGFLWTRKGKLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESG  
STALKAETSERLRTVLLDVTDPEVKRATAQWVKNQVGEKGLWGLINNAGVPGVLAPTDWLTLLEDY  
REPIEVNLFGGLISVTLNMLPLVKKAQGRVINSSVGGRLAIVGGGYTPSKYAVEGFNDSLRRDMK  
AFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEKYIEKSLDKLKGKNSYVNMD  
LSPVVECMDHALTSFLPKTHYAAAGKDAKIFWIPLSHMPAALQDFLLLKQKAE LANPKAV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

## **FIGURE 21**

CTGAGGCCGGCGGTAGCATGGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTGTGCTCGGCG  
CACTCGCTTCCAGCACCTAACACACGGACTCGGACACGGAAAGGTTCTTCTGGGAAGTAAAA  
GGTGAAGCCAAGAACAGCATTACTGATTCCAAATGGATGATGTTGAAGTTGTTATAAATTGA  
CATTCAAGAAATATATTCCATGCTATCAGCTTTAGCTTTATAATTCTTCAGGCGAAGTAAATG  
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAGAATGTGGTAGGTTGGTACAAATTCCGT  
CGTCATTCAAGATCAGATCATGACGTTAGAGAGAGGCTGCTCACAAAAACTTCAGGAGCATT  
TTCAAAACCAAGACCTTGTTCTGCTATTAAACACCAAGTATAAAACAGAAAAGCTGCTACTC  
ATCGACTGGAACATTCTTATATAAACCTCAAAAGGACTTTTCACAGGGTACCTTAGTGGTT  
GCCAATCTGGCATGCTGAACAACGGTTATAAAACTGTATCAGGTTCTGTATGTCCACTGG  
TTTAGCCGAGCAGTACAAACACAGCTCTAAATTTGAAGAAGATGGATCCTTAAAGGAGG  
TACATAAGATAAAATGAAATGTATGCTTCAAGAGGAATTAAAGAGTATATGCAAAAAGTG  
GAAGACAGTGAACAAGCAGTAGATAAAACTAGTAAAGGATGTAACAGATAAAACGAGAAATTGA  
GAAAAGGAGAGGAGCACAGATTCAAGGCAGCAAGAGAGAAGAACATCCAAAAGACCCTCAGGAGA  
ACATTTCCTTGTCAAGGCTTACGGACCTTTTCCAAATTCTGAATTCTTCATTGATGTGTT  
ATGTCTTAAAAAAATAGACATGTTCTAAAGTAGCTGTAACTACAACCACATCTGATGTAGT  
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCTGAAGCTAGTCCAGCTAGTACACCAC  
AAATCTTAAAGCATAAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTA  
GATACACAAGACAACAGATCTAAAGCAAATACTGGTAGTAGTAAACCAAGATAAACATCCAAAAT  
GAGCAGCCCAGAAACAGATGAAGAAAAGATGAAGGGTTGGTGAATATTCAACGGCTC  
CTACATTTGATCTTTAACCTACAAGGAGATTTTATTGGCTGATGGTAAAGCCAAAC  
ATTCTATTGTTTACTATGTGAGCTACTGCACTTACTACAAAGTACTTTCAAACATCA  
TGTTGCACTAATACAGATAACTCTAGTCATTCAACAGTAAAGTACTTTCAAACATCA  
GATGCTTATTCCAAACCTTTTACCTTCACTAAGTTGAGGAGGCTACACAG  
ACACATTCTTGAATTGGAAAAGTGAGACAGGAGCACAGTGGCTCACACCTGTAATCCCAGCACT  
TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGCAACGTATT  
GAGACCATGTCATAAAATAAAATGGAAAAGCAAGAAATAGCCTTATTTCAAAATATGGAAA  
GAAATTATGAAAATTATCTGAGTCATTAAATTCTCCTTAAGTGTAACTTTTAGAAGTA  
CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAATTGCAAAACATCATCT  
AAAATTAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 22**

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLGEVKGEAKNSITDSQMDDVEVVTIDIQKYI  
PCYQLFSFYNSSGEVNEQALKKILSNVKKNVGWYKFRRHSDQIMTRERLLHKNLQEHFSNQDL  
VFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSSEQLGYKTVSGSCMSTGFSRAV  
QTHSSKFFEDGSILKEVHKINEMYASLQEELKSICKVEDSEQAVDKLVKDVNRLKREIEKRRGA  
QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSCKSSCNYNHLDVVDNLT  
MVEHTDIPAEASPASTPQIIKKHALLDLDRWQFKRSRLLDTQDKRSKANTGSSNQDKASKMSSPET  
DEEIEKMKGFGEYSRSPTF

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation sites.**

amino acids 75-79, 322-326

**N-myristoylation site.**

amino acids 184-154

**Growth factor and cytokines receptors family.**

amino acids 134-150

## **FIGURE 23**

GGCACAGCCGCGCGGCCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCCAA  
GCAGCGCGCAGCGAACGCCCGCCGCCACACCCCTCGCGGCCCCGGCGGCGCTGCCACCCCTCCCTCCCTCCCC  
GCGTCCCCGCGCTCGCCGCCAGTCAGCTTGCGGGGTTCGCTGCCCGCGAACACCCGAGGTACCCAGCGCGCTCT  
GCTTCCCTGGGCCGCGCCGCCACGCCCTCCCTGCCCGCCCTGGCACCGGGACCGTTGCC  
CGCGAGGCCAGCTACTTTGCCCGCTCTCCCGCTGCGCTCTCCACCAACTCCAACCTCCCTCCCC  
TCCAGCTCCACTCGCTAGTCCCGACTCCGCCAGCCCTGCCGCTGCCGAGCCGCTTCCCGTCCGGTCCAAA  
GGTGGGAACCGCTCCGGCCCGGCCGACCATGGCAAGGTTGCCGCTGCCGCTTCTGCCACCCCTGGCAGTGCTC  
AGCGCCCGCTGGCTGCCGAGCTCAAGTCGAAAGTTGCTCGGAAGTGCAGCTTTACGTGTCAAAGGCTTC  
AACAAAGAACGATGCCCTCCACGAGATCAACGGTATCATTGAAGATCTGCCCCAGGGTTCTACCTGCTGCTCT  
CAAGAGATGGAGGAGAAGTACGCGTGCAGAAAGTAAAGATGATTCAAAAGTGTGGTCAGCGAACAGTGAATCATTG  
CAAGCTGCTTTGCTTACGTTACAAGAAGTTGATGAATTCTCAAAGAAACTACTTGAAATGCAGAGAAATCCCTG  
AATGATATGTTGTAAGACATATGCCATTATACATGCAAATTCTGAGCTATTAAAGATCTCTCGTAGAGTTG  
AAACGTTACTACGTGGTGGAAATGTAACCTGGAAGAAATGCTAAATGACTCTGGCTCGCCCTCGGAGGGATG  
TTCCGCCCTGGTAACCTCCAGTACCAACTTACAGATGAGTATCTGGAATGTTGAGCAAGTACGGAGCAGCTGAAG  
CCCTTCGGAGATGCTCCCGCAATTGAAGCTCCAGGTTACTCGTGTGTTGTAGCAGCCCTACTTCGCTCAAGGC  
TTAGCGGGTGCAGGAGATGCGTGAAGGCTCCGTGACTGTGAAGCATGTTACAACATGCTCAAACATGAGAGGC  
ATGATCTACTGCTCCACTGCCGGGCTCGTGACTGTGAAGCATGTTACAACATGCTCAAACATGAGAGGC  
TGTTTGGCCAACCAAGGGATCTGATTTGAATGGAACAATTCTCATAGATGCTATGCTGAGGGCAGAGAGGCTA  
GAGGGTCCTTCAACATTGAATCGGTATGGATCCCATCGATGTGAAGATTCTGATGCTATTATGAACATGCAGGAT  
AAATAGTGTCAAGTGTCTCAGAAGGTTTCCAGGGATGTTGAGCCAAAGCCCCAAGCCCCCTCCAGTGGACGAATTCTCGT  
TCCATCTGAAAGTGCCTCAGTGTGCTCAGACCACATACCCCGAGGAACGCCAACACAGCAGCTGGCACT  
AGTTTGGACCGACTGGTTACTGATGTCAGGAGAAACTGAAACAGGCCAGAAATTCTGGCTCCCTCCGAGCAAC  
GTTTGCAACGATGAGAGGATGGCTGAGGAAACGCCAATGAGGATGACTGTTGGAATGSSAAAGGCAAAAGCAGGTAC  
CTGTTGCACTGACAGGAATGGATTAGCCAACCAGGGCAACAACCCAGAGGTCCAGGGTACACCAAGCAAAACAGAC  
ATACTGATCCTCGTCAAATCATGGCTCTCGAGTGATGACCGCAAGATGAAAGATGCAACATGGAACGAGTG  
GACTTCTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGGAGTGGCTGTGAGTATCAGCAGTGCCCTCAGAG  
TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCTGAGAAAGCCGACAGTGTGGTGTCCGTCTGGGCA  
CAGGCTACCTCTCAGTCCTGCTCATCTGTTCTGGTTATGCAAGAGAGAGTGGAGATAATTCTCAAACACTGAG  
AAAAAGTGTCAAAAGTTAAAGGCCAGTTACCTTACCTTCTACCTGAGTTGCTTAAAGTGTGACTTGTGTTCTCATTGAG  
TGGACACAAATGTACAGTTTACTATGTTGCTGAGGAAACGCCAATGTTAAACGGTGGCTAACAGTGTAGGTACAGAA  
AGGAAAAGGGACTGTGCAATTGAGTTGTTCTGCTCCCAACCATGTTAAACGGTGGCTAACAGTGTAGGTACAGAA  
CTATAGTTAGTTGTCATTGATGTTTACTCTTACCTCTTACCTTCTGTTGATGTTTTCTCATTTCGTTGTTGGGTT  
TTTTTTCCAACGTGATCTCGCCTTGTCTTACAAGCAAACCGGGCCCTTCTGGCACGTAACATGTACGTATT  
TCTGAAATATTAATAGCTGTACAGAAGCAGGTTTATTTATCATGTTATCTTAAAGAAAAGCCAAAAGC

## **FIGURE 24**

MARFGLPALLCTLAVLSAALLAAELKSCHKSCSEVRRILYVSKGFKNDAPLHEINGDHLKICPQGST  
CCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSNDMFVKTYGH  
LYMQNSELFKDLFVELKRYYVVGNVLEEMLNDFWARLLERMFRVLVNSQYHFTDEYLECVSKYTE  
QLKPFGDVPRKLKLQVTRAFVAARTFAQGLAVAGDVSKVSVNPTAQCTHALLKMIYCSHCRL  
VTVKPCYNYCSNIMRGCLANQGDLDFEWNNFDAMLMVAERLEGPPNIESVMDPIDVKISDAIMN  
MQDNSVQVSQKVFCQCGPPKPLPAGRISRSISESAFSARFRPHHPEERPTTAAGTSLDRLVTDVK  
EKLKQAKKFWSLPSNVCNDERMAAGNGNECDCWNGKGKSRYLFATVGNGLANQGNNPEVQVDTS  
KPDILILRQIMALRVMTSKMKNAYNGNDVDFFDISDESSGEKGSGSCCEYQQCPSEFDYNATDHAG  
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

**Important features:**

**Signal peptide:**

amino acids 1-22

**ATP/GTP-binding site motif A (P-loop).**

amino acids 515-524

**N-glycosylation site.**

amino acids 514-518

**Glycosaminoglycan attachment sites.**

amino acids 494-498, 498-502

**N-myristoylation sites.**

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

**Glycans proteins.**

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

## **FIGURE 25**

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC  
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTCATTATATTCTTCAGCAACT  
TACAGCTGCACCGACAGTTGCGGATGAAAGTTCTAATCTTCCCTCCTGTTGCTGCCACTAA  
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGTCGCCAGAGGCCACAGGGACCGAGGC  
CAGGCTCTAGGAGATGGCTCCAGGAAGGCCAAGAATGTGAGTGCAAAGATTGGTCCTGAG  
AGCCCCGAGAAGAAAATTATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCCTGTGATCATT  
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACACAGAAAGCCAACAAGCATTCCAGA  
GCCTGCCAGCAATTCTCAAACAATGTCAGCTAAGAAGCTTGCTGCTGCCTTGTAGGAGCTCTG  
AGCGCCCACCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAAGACACTC  
TTCTTCTCCCACCTCACTCTCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAGCA  
TGTTTTCAAGATCATTGTTGCTCTCTAGTGCTTCTCTCGTAGTCTAGCCT  
GTGCCCTCCCTAACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCC  
AGCTAGTGTCATTAAACCTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTT  
AAATGTCAAAAAAAAAAAAAAAA

## **FIGURE 26**

MKVLISSLLLLPLMLMSMVSSSLNPGVARGHDRGQASRRWLQEGGQECECKDWFLRAPRKFM  
TVSGLPKKKCPCDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 27-33, 46-52

## **FIGURE 27**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAGCCAGTCCCCAGCGGAAGCACAGCTCAG  
AGCTGGTCTGCCATGGACATCCTGGTCCCACCTCTGCAGCTGCTGGTGTGCTTACCTGCC  
CCTGCACCTCATGGCTCTGCTGGCTGCTGGCAGCCCCGTGCAAAGCTACTTCCCACCTGA  
TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTTCAGCCAG  
ATAAAGGGCTTACAGGAGCCTCCGGAAAGTGGCCCTACTGGAGCTGGCTGCGGAACCGGAGC  
CAACTTCAGTTCTACCCACCGGGCTGCAGGGCACCTGCCTAGACCCAAATCCCCACTTGAGA  
AGTTCCGTACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTGTGGTGGCTCCT  
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGTGCACTCTGGTGTG  
CTCTGTGCAGAGCCAAGGAAGGTCTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTG  
TCTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGCCTTCATGTGGCAGCAAGTTTC  
GAGCCCACCTGAAACACATTGGGATGGCTGCTGCCTCACAGAGAGACCTGGAAGGATCTGA  
GAACGCCAGTTCTCGAAATCCAATGGAACGACAGCCCCCTCCCTGAAGTGGCTACCTGTTG  
GGCCCCACATCATGGGAAAGGCTGCAAACAATCTTCCAAGCTCCAAGGCACTCATTTGCTCC  
TTCCCCAGCCTCCAATTAGAACAGCCACCCACCAGCCTATCTATCTTCACTGAGAGGGACCTA  
GCAAGATGAGAGAACATTCACTGTGACAGCTACTAGTCCCTCTCCCCAACCTCTGCCAGGGC  
AATCTCTAACTTCAATCCGCCCTCGACAGTGAAAAGCTCTACTTCTACGCTGACCCAGGGAGG  
AAACACTAGGACCCGTGTATCCTCAACTGCAAGTTCTGGACTAGTCTCCCAACGTTGCTC  
CCAATGTTGCCCTTCCCTCGTCCATGGTAAAGCTCTCTCGCTTCCCTGAGGCTACAC  
CCATGCGCTCTAGGAACGTGGTACAAAAGCTCATGGTGCCTGCATCCCTGCCAACGCCCCCTGAC  
CCTCTCTCCCCACTACCACCTTCTCGAGCTGGGGGACCAAGGGAGAATCAGAGATGCTGGGG  
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATATTTTAATAAATAGACGAA  
ACCACG

## **FIGURE 28**

MDILVPLLQLLVLLTLPLHLMALLGCWQPLCKSYFPYILMAVLTPKSNRKMESKKRELFSQIKGL  
TGASGKVALLELGCCTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM  
RQLADGSMDVVVCTLVLCVQSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFMWQQVFEPTW  
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFPSSKALICSFPSL  
QLEQATHQPIYLPLRGT

**Important features:**

**Signal peptide:**

amino acids 1-23

**Leucine zipper pattern.**

amino acids 10-32

**N-myristoylation sites.**

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

## **FIGURE 29**

CAATGTTGCCTATCCACCTCCCCAAGCCCCTTACCTATGCTGCTGCTAACGCTGCTGCTGCT  
GCTGCTGCTGCTAAAGGCTCATGCTGGAGTGGGACTGGTCGGGCCAGAAAGTCTCTCTG  
CCACTGACGCCCCCATCAGGGATTGGGCCTCTTCCCCCTCCTTCTGTGTCCTGCCTCAT  
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGAGAAAGTGGGGATGGGCTA  
AGAAAGCTGGGAGATAGGGAACAGAACAGAGGGTAGTGGGTGGGCTAGGGGGCTGCCTTATTTAAA  
GTGGTTGTTATGATTCTTATACTAATTATACAAAGATATTAAGCCCTGTTCATTAAGAAATT  
GTTCCCTCCCTGTGTTCAATGTTGTAAGATTGTTCTGTGIAAATATGTCTTATAATAAAC  
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 30**

MLLLTLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCQAQPRG  
EGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

**FIGURE 31**

GTTCCTGAACTTCCCTCAACTATACCCACAGTC  
CCTCCAAGCAAGTCATTCCCTTATTTAACCGATGTG  
ATTTGCATCTGTTTGATAAATGATGTTGACACCCT  
GAAGAGATAACAATCCTGGCCTGTGTATCCTCGC  
TTTCAGATTTCATCACCAACCCCTCTGGTT  
TGTCTGCGGTGTTTATGGTGGCTGTATTATGACT  
CAGAAAGGGAAAATATGAAGTGCCTGCTGGGTT  
CTGCTCGTCTGATTGGTCTCAGAAAGAGAATAA  
AAATAAAGCCATCAGCAGTGCCTCCCTGCTGTT  
TTTCTCTGGGTCCCTGGGTGGCTGTGCTGAG  
ATGGAAAGGCCAAGTGAATATAAGCCCC  
AATTGGCCTCATCTGGACTAGTGAATT  
TGGTTACTTGTATTCAACAGAAGTAAAAA  
TCCATTCTCTTCTTACCATCAAGGAACCG  
GATTCCGAGAATCATTGT  
CCAGGTACCTGTTCCGATGCTGCTACT  
AACACAGAATGC  
ATTCAAATCTTGT  
TTTTCTAGGAAAGGTGTTAGTGGTGT  
AATCGGGCATTCCAGGTG  
CCATAGTTTTTATCTGT  
TGGAAACAAATGATGG  
AAAAGGAGCAACAAAT  
GGGAACAGAACTCC  
TCCCT  
TCTAAGAGCCATT  
TTAAAAGAC  
CTAATAAAC  
CTTCC  
CTCAAAA

## **FIGURE 32**

MSGRTDTILGLCILALALSLAMMFTFRFITTLLVHIFISLVLGLLFVCGLVWWLYYDYNLDLSIE  
LDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQPLWTFA  
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQMTIA  
GAVVTCYFNRSKNDDPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMYMQLKEQQHG  
ALSRYLFRCYCFCWCLDKYLLHLNQNAYTTAINGTDFCTSAKDAFKILSKNSHFTSINCFGD  
FIIFLGKVLCFTVFGGLMAFNYNRAFQWAVPLLVAFFAYLVAHSFLSVFETVLDALFLCFA  
VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

**Important features:**

**Signal peptide:**

amino acids 1-20

**Putative transmembrane domains:**

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

**N-glycosylation sites.**

amino acids 204-208, 295-299, 313-317

**N-myristoylation sites.**

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

## **FIGURE 33**

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTCTGGACCTCCCTGTTCTCCTTAGA  
ATAATTGTATGGGATTGTGATGCAGGAAAGCTAAGGGAAAAAGAATATTCAATTCTGTGTGGT  
GAAAATTTTGAAAAAAAATGCCTCTCAAACAAGGGTGTCAATTCTGATATTTATGAGGAC  
TGTTGTCTCACTATGAAGGCATCTGTTATGAAATGTCCTGTTGCTGGTACTGGAGTAC  
ATTCAAACAAGAACGGCAAAGAAGATTAAAGGCCAAGTCAGTGTGCCTCAGATCAACTGC  
GATGTCAAAGCGGAAAGATCATCGATCCTGAGTCATGTGAAATGTCAGCAGGATGCCAAGA  
CCCCAAATACCATGTTATGGCACTGACGTGATGCATCCTACTCCAGTGTGTGGCGCTGCCG  
TACACAGTGGTGTGCTGATAATTCAAGGAGGGAAAATACTTGTTCGGAAGGTTGCTGGACAGTCT  
GGTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTTATCCCTACCACGATGGAGAGAATCCTT  
TATCGCTTAGAAAGTAAACCCAAAAGGGTGTAAACCTACCCATCACCTTACATACATCAT  
CGAAAAGTCCAGTCCCAGCAGGTGAGACCACAAAAGCCTATCACAGGCCACCTATTCCAGGG  
ACAACGTGACAGCCGGTCACTCTGATGCAGCTCTGGCTGTCAGTCAGCTGTGGCCACCCCCAC  
CACCTTGCCAAGGCCATCCCCCTCTGTCGCTTACCCACGATCCCCAGACACAAATCAGTGG  
GCCACAGGAGCAGGAGATGGATCTGGTCCACTGCCACCTACAAAGCAGCCAAAAGGCC  
AGAGCTGATCCAGGTATCCAAAGGCAAGATCCTCAGGAGCTGCCTCCAGAAACCTGTGGAGC  
GGATGTCAGCCTGGGACTTGTCCAAAAGAGAATTGAGCACAGCTTGGAGCAGTATCCC  
TGGGAGATCCAAACTGCAAATGACTTGTGTTTAATTGATGGAGCACCAGATTGGCAAA  
CGGCATTCCGAATCCAGAAAGCAGCTCTGGCTGATGTGCCCCAGCTCTGACATTGGCCCTGC  
CGGTCCACTGATGGGTGTTGTCAGTATGGAGACAACCTCTGACTACTTAAACCTCAAGACAC  
ACACGAATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGGACTTCTAAT  
GTAGGTCGGGCCATCTCTTGACCAAGAACATTCTTICCAAGCCATGGAAACAGAACGG  
GGCTCCAATGTGGTGGTGGTGTGGTGGATGGCTGGCCACGGACAAAGTGGAGGAGGCTCAA  
GACTTGCAGAGAGTCAGGAATCAACATTCTTCATCACCAATTGAAGGTGCTGCTGAAAATGAG  
AAGCAGTATGTGGTGGAGCCAACTTGTGCAAACAAGGCCGTGTCAGAACAAACGGCTTACTC  
GCTCCACGTGCAAGAGCTGGTTGGCCTCCACAAGACCCCTGCAAGCCTCTGGTGAAGGGCTGCG  
ACACTGACCGCCTGGCCTGCAAGCAAGACCTGCTGAACCTGGCTGACATTGGCTCGTCA  
GGCTCCAGCAGTGTGGGAGGGCAACTTCCGACGGCCTCCAGTTGTGACCACTCACCAA  
AGAGTTGAGATTTCGACACGGACACGCGCATGGGGCGTGCAGTACACTGACAGCGGC  
TGGAGTTGGGTTGCAAGTACAGCAGCAAGCCTGACATCCTCAAGCCATCAAGAGGGTGGC  
TACTGGAGTGGTGGCACAGCACGGGGCTGCCATCAACTTCCGCTGGAGCAGTCTCA  
GTCCAAGCCCAACAAAGAGGAAGTTAATGATCTCATCACCGACGGGAGGTCTACGACGAGCT  
GGATCCAGCCATGGCTGCCCATCTGAAGGGAGTGTACACCTATGCGATAGGCGTTGCCTGGCT  
GCCCAAGAGGAGCTAGAAGTCATTGCCACTCACCCGCCAGAGACCAACTCCTTCTTGTGGACGA  
GTTTGACAAACCTCATCACTGATGTCCCCAGGATCATCCAGAACATTGTCAGAGTTCAACTCAC  
AGCCTCGGAACTGAATTCAAGAGCAGGCAGAGCACCAGCAAGTGTCTTACTAATGACGTGTT  
GGACCAACCCACCGCTTAATGGGGCACGCACGGTGCATCAAGTCTGGCAGGGCATGGAGAAC  
AAATGCTTGTATTATTCTTGCCATCATGCTTTTCATATTCCAAAATCTGGAGTTACAAGA  
TGATCACAAACGTATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTACAT  
TTTGACAAATTGTTCTAAAATAATGTTGGAATACAGTGCAGCCCTACGACAGGCTTACGTAG  
AGCTTTGTGAGATTAAAGTGTATTCTGATTTGAAACTCTGTAACCCCTCAGCAAGTTTCAT  
TTTGTCATGACAATGTAGGAATTGCTGAATTAAATGTTAGAAGGATGAAAAATAAAAAAAAA  
AAG

## **FIGURE 34**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINC DVKAGKIIDPEFIVKCPAG  
CQDPKYHVGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWR  
ESFIVLESKP KKGVTYPSALTYSSSKPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVA  
TPTTLPRPSPSAASTTSIPR PQSVGHRSQEMDLWSTATYTSSQNRPADPGIQRQDPSGAAFQKP  
VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI  
GPAGPLMGVVQYGDNPATHFNLKHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN  
RSGAPN VVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG  
FYSLHVQSWFGLHKT LQPLVKRVCDTRLACSKTCLNSADIGFVIDGSSSVGTGNFR TVLQFVTN  
LTKEFEISDTDTRIGAVQYTYEQRLEFGFDKYSSKPDILNAIKR VGYWSGGTSTGAAINF ALEQL  
FKKS KPNKRKLMILITDGRSYDDV RI PAMA AHLKG VITYAIGVAWA A QEELEVIATHPARDHSFF  
VDEF DNLHQYV PRIQNICTEFNSQPRN

**Important features:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 181-200

**N-glycosylation sites.**

amino acids 390-394, 520-524

**N-myristoylation sites.**

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,  
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

**Amidation site.**

amino acids 304-308

## **FIGURE 35**

CCGAGCACAGGAGATTGCCTGCGTTAGGAGGTGGCTGCCTGTGGAAAAGCTATCAAGGAAGAAATTGC  
CAAACCATGTCTTTTCTGTTTCAGAGTAGTTACAACACAGATCTGAGTGTTTAATTAAGCATGGAAT  
ACAGAAAACAACAAAAACTTAAGCTTAATTCTATCTGGAATTCCACAGTTCTTAGCTCCCTGGACCC  
GGTTGACCTGTTGGCTCTCCCGCTGGCTGCTATCAGCTGGTCTCCGACTACTCACCCGAGTGT  
AAGAACCTTCGGCTCGCGTCTGAGCTGCTGTGGATGGCCTCGGCTCTGGACTGTCCTCCGAGTA  
GGATGTCACTGAGATCCCTCAAATGGAGCCTCTGCTGTCACTCCTGAGTTCTTGTATGTGGTAC  
CTCAGCCCTCCCCACTACAATGTGATAAGACCGTGAACGGTACTGGATGTACTCTATGAGTATGAGCGATT  
CAGACAAGACTTCACTTCACACTCGAGAGCATTCAAACACTGCTCTCATCAAATCCATTCTGGTCATT  
TGGTGACCTCCCACCCCTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTGGGGTGAAGAAAGTCT  
TGGTGGGGATATGAGGTTCTTACATTCTTATTAGCCAAGAGGCTGAAAGGAAGACAAATGTTGGC  
ATTGTCTTAGAGGATGAAACACCTCTTTATGGTACATAATCCGACAAGATTAGACACATATAATA  
ACCTGACCTTGAAACCATTATGGCATTCAAGGTGGTAACTGAGTTTCCCCAATGCCAAGTACGTAATG  
AAGACAGACACTGATGTTTCAATACTGGCAATTAGTGAAGTATCTTAAACCTAAACCACTCAGA  
GAAGTTTTCACAGGTTATCCTCTAATTGATAATTATTCTATAGAGGATTTACCAAAAAACCCATATT  
CTTACCAAGGAGTATCCTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTATATAATGTCAGAGAT  
TTGGTGCAAGGATCTATGAAATGATGGTCACGTAACCCATCAAGTTGAAGATGTTATGTCGGGAT  
CTGTTGAATTATAAAAGTGAACATTCAATTCCAGAAGACACAAATCTTTCTTCTATAGAATCC  
ATTGGATGTCGTAACGTGAGACGTGATTGCAGCCCATTGGCTTTCTCCAAGGAGATCATCATT  
TGGCAGGTGTCAGGATCTATGAAATGATGGTCACGTAACCCATTAACTTCACATTCTACAAAAGCCTAGAAGGACAG  
GATACTGAACTGAAACTCATGAAAACCCAGACTGGAGACTGGAGGGTTACACTGTGATTATTAGTCAGG  
CCCTCAAAGATGATATGTGGAGGAATTAAATATAAGGAATTGGAGGTTTGCTAAAGAAATTAGG  
ACCAAACAATTGGACATGTCATTCTGTAGACTAGAATTCTTAAAGGGTTACTGAGTTATAAGCTCA  
CTAGGCTGAAAAACAAACATGTAGAGTTATTGAAACAATGTAGTCACTTGAAGGTTGTGTA  
TATCTTATGTGGATTACCAATTAAATATAATGTAGTTCTGTGTCACAAACTCTTCACTGAAGTTATA  
CTGAACAAATTTCACCTGTTGGTCATTATAAGTACTTCAGATGTCAGTGTGCTGGCTTACAGTTATT  
ATTATTTAAATTACTTCACATTGTGTTAAATGTTGACGATTCAACAGATAAAAGGATAG  
TGAATCATTCTTACATGCAAACATTCCAGTTACTTAACGTGATCAGTTATTGATAACATCACTCCA  
TTAATGAAAGTCATAGGTCAATTGCAATCTCAGTAATCTTGGACTTGTAAATATTACTGTGGT  
AATATAGAGAAGAATTAAAGCAAGAAATCTGAAAA

## **FIGURE 36**

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPIYRQDFHF  
TLREHSNC SHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSSWWGYEVLTFFLLGQEAEKEDKMLA  
LSLEDEHLLYGDII RQDFLDTYNNLT LKTIMA FRWVTEFCPNAKYVMKTDTDVFINTGNLVKYLL  
NLN HSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMS RDILV PRIYEMMGHV  
KPIKFEDVYVGICLNLLKVNIH IPE DTNLFFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR  
NTTCHY

**Important features:**

**Type II transmembrane domain:**

amino acids 20-39

**N-glycosylation sites.**

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

**Glycosaminoglycan attachment site.**

amino acids 239-243

**Ly-6 / u-PAR domain proteins.**

amino acids 23-37

**N-myristoylation site.**

amino acids 271-277

## **FIGURE 37**

CGCTCGGCCACCAGCCGGCAAGGATGGAGCTGGGTTGCTGGACGCAGTGGGCTACTTTCTTCAGCTCCTTCATC  
TCGTCCCTGCCAAGAGAGTACACAGTCATAATGAAGCTGCCCTGGAGCAGAGTGGAAATATCATGTCGGAGTGCTGTG  
AATATGATCAGATTGAGTGCCTGCCCCGGAAAGAGGAAAGTCTGTTGAGTGGGTTATACCATCCCTGCTGCAGGAATGAGGAGAA  
TGAGTGTGACTCCCTGCCCTGATCCACCCAGGTTGACTCATCTTGAAAAGTCAGAGCTGCCGAATGGCTCATGGGGGGT  
ACCTTGGAGACTCTATGTGAAGGGGTCTACTGTGAGAGTGCAGAGCTGGAGGGAGACTGCATGCCATGTG  
GCCAGGTTCTGCGAGCCCCAAAGGGTCAAGATTTGTTGAAAGCTATCCCCTAAATGCTCACTGTGAATGGACCATTGATGC  
TAAACCTGGGTTGTCATCCAACTAAGATTGTCATGTTGAGTCTGGAGTTGACTACATGTGCCAGTATGACTATGTTGAG  
GTTCGTGATGGAGACAACCGCGATGCCAGATCATCAAGCGTGTCTGGCAACGAGCGGCCAGCTCCATCCAGAGCATAG  
GATCCTCACTCCACGTCCTCTTCACTCCGATGGCTCCAAGAATTTGACGGTTCCATGCCATTATGAGGAGATCACAGC  
ATGCTCCTCATCCCCCTGTTCCATGACGGCACGTCGCTTGCAGAACGGCTGATCTTACAAGTGTGCTGCTGGCAGGC  
TATACTGGGCAGGCCTGTTGAAAATCTCTTGAAGAAAGAAAATCTGTCAGACCCCTGGGGCCAGTCATGGGTACAGAAAAA  
TAAACAGGGGGCCCTGGGTTATGACAGGAGCCATGCTAAATGGCACCGTGTGTCTTTGTAACAACCTCTATGTT  
TCTTAGTGGCAATGAGAAAAGAATGGCAGCAGAATGGAGAGTGGTCAAGGAAACAGCCCATCTGCATAAAAGCCTGCCGA  
GAACCAAAGATTTCAGACCTGGTCAAGAGGAGACTCTCCGATGCAAGGAGACACCATTACACCACCTAT  
ACTCAGGCCCTCAGCAAGCAGAAACTGCAGAGTCCCTACCAAGAACGCCCTCCCTGGAGATCTGCCATGGG  
ATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCACTCACCCTCTACCGCCGCTGGCAGCAGCAGGAGGACATGT  
CTGAGGACTGGGAAGTGGAGTGGCGGGCACCATCCTGCATCCCTATCTGCGGGAAATTGAGAACATCACTGCTCCAAAAGA  
CCCAAGGGTTGCGCTGGCGTGGCAGGCCATCTACAGGAGGACAGCGGGGTGCATGACGGCAGCCTACAAAGGGAGC  
GTGTTCTAGTCTGCAACGGTGCCCTGGTGAATGAGGCACTGTGGTGGTGGCTGCCACTGTGTTACTGACCTGGGAAG  
GTCACCATGATCAAGACAGCAGACCTGAAAGTTGGGAAATTCTACCGGGATGACCGGGATGAGAACCATCC  
AGACCTACAGATTCTGCTATCTGCATCCAACTATGACCCCATCTGCTGATGACATGCCATCTGAAAGCT  
CCTAGACAAGGCCGTATCAGCACCCGAGTCCAGGCCATCTGCTCGCCAGTGGGATCTCAGCAGTCTCCAGGAG  
TCCCACATCACTGTGGCTGGCTGGAATGCTCTGCAGCAGTGAGGAGGCCCTGGCTCAAGAACGACACACTGCGCTCTGGG  
TGGTCAGTGTGGTGGACTCGCTGCTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGAGTGTCACTGATAACATGTT  
CTGTCGCAGCTGGGAACCCACTGCCCCCTCTGATATCTGCACTGCAAGACAGCAGGAGCATCGCGCTGTGCTTCCGGGA  
CGAGCATCTCTGAGCCACGCCTGGCATCTGATGGACTGGTCACTGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA  
CTGCCCCACCAAGGTGCTGCCCTTTAAAGACTGGATTGAAAGAAATGAAAATGACCATGCTCATGCACTCTTGAAG  
TGTTCTGTATATCGCTGTACGTGTCATTGGTCAAGGACTGTGAAGGGTGAAGTAGACCTCATTGCTGGTAGGCTGATGCCGCTCCA  
CTACTAGGACAGCCAATTGGAAGATGCCAGGGCTGCAAGAAGTAAGTTCTCAAGAACAGACCATATACAAAACCTCTCCA  
CTCCACTGACCTGGTGGCTTCCCAACTTCACTGTTATACGAATGCCATCAGCTTGACCCAGGGAGATCTGGCTTCACTGAG  
GCCCTTTGAGGCTCAAGTTCTAGAGAGCTGCCCTGGGACAGGCCAGGGCAGCAGAGCTGGGATGTTGCTGATGCCCT  
TGTGTACATGCCACAGTACAGTCTGGCTTTCTCCCCATCTGTACACATTAAATAAAATAAGGGTGGCTTCA  
GAACTACAA  
AA

## **FIGURE 38**

MELGCWTQLGLTFLQLLLSSLPREYT VINEACPGAEWNIMCRECC EYDQIECVCPGKREVVGYT  
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWYGGDCMRCGQ  
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGQII  
KRVC GNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC  
ACLAGYTGQR CENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSGNE  
KRTCQ QNGEWSGKQPIKACREP KISDLVRRRVLPQM QVSRETPLHQLYSAAFSKQKLQSAPTK  
KPALPF GDLPMGYQHLHTQLOQYECISP FYRLGSSRRTCLRTGKWSGRAPSCI PICGK IENI TAP  
KTQGLRWPWQAAIY RRTSGVHDGSLHKGA WFLVC SGALVNERTVVVAHCVTDLGKV TMK TADL  
KVVLGKFYR DDDRDEKTIQSLQISAIILHPNYDPILL DADIAILKLLDKARI STRVQPI CLAASR  
DLSTS FQESHITVAGWNVLADVRS PGFKNDTLRGV SVVDSLLCEEQHEDHGI PVS VTDNMFC A  
SWEPTAPS DICTAETGGIAAVSF PGRASPEPRWHLMGLV SWSYD KTC SHRLSTAFTKVL PFKDWI  
ERNMK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**EGF-like domain cysteine pattern signature.**

amino acids 260-272

**N-glycosylation sites.**

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

**N-myristoylation sites.**

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,  
474-480, 491-497, 638-644, 666-672

**Amidation site.**

amino acids 56-60

**Serine proteases, trypsin family.**

amino acids 489-506

**CUB domain proteins profile.**

amino acids 150-167

## **FIGURE 39**

GGTTCCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTACGGGCCGTGATTATTAACGTGGCTTAATC  
TGAAGGTTCTCAGTCATAATTCTTGATCTACTGATTGTGGGGCATGGCAAGGTTGCTTAAAGGAGCTTGGCTGG  
TTGGGCCCTTGTAGCTGACAGAAGGTGCCAGGGAGAATGCAGCACACTGCTCGAGAATGAAGGCCTTCTGTTGC  
TGGCTTGCCCTGGCTCAGCTGCTAACTACATTGACAATGTGGCAACCTGCACCTCTGTATTCAAAGACTCTGTA  
AAGGTGCTCCCACGGCCTGACCAAAGATAGGAAGAGGCCTCACAAAGATGGCTGTCCAGACGGCTGTGAGGCC  
TCACAGCCACGGCTCCCTCCCCAGAGGTTCTGCAGCTGCCACCCTCCTTAATGACAGACGAGCCTGGCTAGACA  
ACCCCTGCCTACGTGTCCCTGGCAGAGGACGGCAGGCCAGCAATCAGCCAGTGGACTCTGGCCGGAGCAACCGAACTA  
GGGCACGGCCCTTGAGAGATCAGTATTAGAACGAGATCATTAAAAAAATTCAGGCTTGACTGTTCTCGAA  
GGACAAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGGGCAGGGAAATTCTGAAAACACCACTGCCCTGAAG  
TCTTTCCAAGGTTGTACCCACCTGATTCCAGATGGTAAATTACAGCATCAAGATCAATCAGTAGATCCCAGTGAAGA  
GCCCTCTCATTTAGGCTGGTGGAGGTAGCAGAACCCCCACTGGTCCATATCATTATCCAACACATTTATCGTATGGG  
TGATGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGCCCTC  
ACAACATACGCTGTGCGTCTCCCTGCCAGCCCTGCCAGGTGCTGGCTGACTGTGATGCGTAACAGAAGTCCGCA  
GCAGGAACATGGACAGGCCCGGATGCCCTACAGACCCCGAGATGACAGCTTCTGATTCTAACAAAAGTAGCC  
CCGAGGAGCAGCTTGGAAATAAAACTGGTGCAGGAGATGACCGTGTGTTAGCCATCAATGGACATGATCTCGATATGGCA  
GTGTTGGCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTCGATATGGCA  
GCCAGAAAAGTGCAGGCTCATCTGATTCAAGGCCAGTGAAGACGTGTTACCTCGTGTCCCGCCAGGTTCCGAGC  
GGAGCCCTGACATCTTCAGGAAGCCCGCTGGAAACAGCAATGCCAGCTGGTCCCCAGGGCAGGGAGAGGACAA  
CTCCCAAGCCCTCCATCCTACAAATTACTGTGATGAGAAGGTGGTAAATATCCAAAAGACCCGGTGAATCTCTG  
GCATGACCGTGCAGGGGAGCATCACATAGAGAATGGGATTGCTATCTATGTCATCAGTGTGAGCCGGAGGAG  
TCATAAGCAGAGATGAAAGAATAAAAACAGGTGACATTGTTGATGTTGAGTGGGATGGGTCGAACGTGACAGAGGTGAGCC  
GGAGTGGCAGTGGCATTATTGAAAAGAACATCATCCTCGATAGTACTCAAAGCTTGGAGTCAAAGAGTATGAGC  
CCCAGGAAGACTGCAGCAGCCAGGCCCTGGACTCCAACACACATGCCCCACCCAGTGACTGGTCCCATCCT  
GGGTGATGTGGCTGGAATTACCACGGTGTGTTGATAACTGTAAAGATATTGATTACGAAGAAAACAGCTGGAAGT  
TGGGCTCTGATTGAGGAGTTATGAGAATACATGAAACAAACCTTTTCTGATCAATCATTGTAAGGAA  
CACAGCATAATGATGGAAGAATTAGATGTGGTATATTCTCTGCTGTCATGGTAAAGTACATCAGGAATGA  
TACATGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTCTGGCTGGCACTT  
TTTATAAGATCAATGATGGTCAGAGGAAACAGAAAATCACAAATAGGCTAAAGTGAACACTATATTATC  
TTGTCAGTTTATATTAAAGAAGAATACATTGTTAAAGGAAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTT  
ACACCTCAGAAAATATGATTCCAAAAAAATTAAACTACTAGTTTTTCAGTGTGGAGGATTCTCATTACTCTAC  
AACATTGTTATATTCTTCTATTCAATAAAAGCCCTAAACAACTAAAATGATTGATTGATACCCACTGAATT  
CAAGCTGATTAAATTAAATTGGTATATGCTGAAGTCTGCCAAGGGTACATTATGCCATTAAATTACAGCT  
AAAATTTTAAATGCTGAGAACGTTGCTTCAACAAAGAATAAATTTTCAAGAAGTAAA

## **FIGURE 40**

MKALLLLVLPWLSPTYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPDCASLTATAPS  
PEVSAAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDGRSNRTRARPFERSTIRSRSFKKINR  
ALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDPSESLSIRLV  
GGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNMGDISNVPHNAYAVRLLRQPCQVLWLTV  
REQKFRSRNNGQAPDAYRPRDDS FHVILNKSSPEEQLGIKLVRKVDEPGVFI FNVLDDGVAYRHG  
QLEENDRVLAINGHDLRYGSPEAAHLIQASERRVHLVVSQRSPDIFQEAGWNSNGSWSPG  
PGERSNTPKPLHPTITCHEKVNNI QKD PGESLGMTVAGGASHREWDLPIYVISVEPGGVISR DGR  
I KTGDILLNVDGVELTEVRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPP  
SDWSPSWVMWLELPRLCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG  
RIRC GDILLAVNGRSTSGMIHA CLR LLKELKG RITLTIVSWPGTFL

**Important features:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-112, 157-161, 289-293, 384-388

**Tyrosine kinase phosphorylation sites.**

amino acids 433-441, 492-500

**N-myristoylation sites.**

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,  
467-473, 603-609

## **FIGURE 41**

ACCAGGCATTGTATCTCAGTTGTCATCAAGTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT  
CTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTACAGTAATAAAACATGGGCTTCAACCTGACT  
TTCCACCTTCCTACAATTCCGATTACTGTTGCTGTTGACTTTGTGCCCTGACAGTGGTGGGTGGC  
CACCAAGTAACTACTTCGTTGGGCCATTCAAAAGAGATTCTAAAGCAAAGGAGTTCATGGCTAATTCC  
ATAAGACCCCTCATTGGGAAGGGAAAAACTCTGACTAATGAAGCATTCCACGAAGAAGGTAGAAGCTT  
GACAACGTGCTTCTGTGTCTCCCTACCTCAGAGGCCAGAGCAAGCTATTCAAACCAAGATCTCAC  
TTTGGAGAGGGTACAGGCAGAAATCCAAAGTGTCCAGAGGCCGGTATGCCCTCAGGAATGTAAG  
CTTTACAGAGGGTCGCCATCCTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAA  
CATCTGCATCCCTCCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTATCCACCAGGCTGAAGG  
TAAAAAGTTAACGAGCAAACCTCTGAATGTGGGCTATCTAGAAGCCCTAAGGAAGAAAATTGGG  
ACTGTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTACAAGTGTGAGGAG  
CATCCCAAGCATTGGTGGTGGCAGGAACAGCACTGGTACAGGTTACAGTGGATATTGG  
GGGTGTTACTGCCCTAACAGAGAGCAGTTTCAAGGTGAATGGATTCTCTAACAAACTACTGGGAT  
GGGGAGGCAGACGGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTCCCGCCCCCTG  
CCTGAAGTGGTAAATATAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG  
GATGAAGCTCTTACACCAAGTGTACGAGCTGGAGAACAGATGGTGAAGTGGATTCTGGTCTTATAAAT  
TAGTATCTGTGGAACACAATCCTTATATATCAACATCACAGTGGATTCTGGTGGTGCATGACCC  
TGGATCTTGGTGAATGGAAAGAACTGATTCTTGTGCAATAATTGGCCTAGAGACTTCAA  
ATAGTAGCACACATTAAGAACCTTACAGCTCATTGTTGAGCTGAATTTCCTTTGTATTCT  
TAGCAGAGCTCCTGGTGAATGGTGAAGTGGATTCTTGTGCAATAATTGGCCTAGAGACTTCAA  
CATGAGGGTTAAATATTGAATATGGTAACTGAGGACTTTATATAAAAGGATGACTCAAAGGATAA  
AATGAACGCTATTGAGGACTCTGGTGAAGGAGATTATTAAATTGAAGTAATATATTATGGGAT  
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACAGAGTTCTCGTCCAAGGTAGAA  
AGGTACGAAGATAACAATACTGTTATTCACTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTCAAGGT  
GAGAAGGCCTCACAAAGAGGGAGAAAAGGCAGCAATCAGGACACAGTGAACATTGGGAATGAAGA  
GGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAGCAGTAGCTGAGCTGGTGCAGGTGCTGATAGC  
CTTCAGGGAGGACCTGCCAGGTATGCCCTCAGTGTGATGCCACCAGAGAAATACATTCTTATTAGT  
TTTAAAGAGTTTGTAAAATGATTTGTACAAGTAGGATATGAATTAGCAGTTACAAGTACAT  
ATTAACATAATAATATGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAGCAAA

## **FIGURE 42**

MGFNLTFHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLIGKGKTLTN  
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH  
RNREKHLMLLEHLHPFLQRQOLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFIFHDV  
DLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTLSREQFFKVNGFSNNYWGWGGED  
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV  
SVEHNPLYINITVDFWFGA

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 4-8, 220-224, 335-339

**Xylose isomerase proteins.**

amino acids 191-202

### **FIGURE 43**

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACCGATGGCACTGAGCTCCCAGATCTGGG  
CCGCTTGCCTCCTGCTCCTCCTCCCTGCCAGCCTGACCAGTGGCTCTGTTTCCCACAACAG  
ACGGGACAACCTGCAGAGCTGCAACCCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCAT  
GTTCCAGAGGCAGAAGGAGGCAGACACCCACTCCCCATCTGCATTTCCTGCTGCGGCTGTC  
ATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTGCCCCGTCCCCTCCC  
TTCCTTATTATTCCTGCTGCCAGAACATAGGTCTTGAATAAAATGGCTGGTTCTTTGTT  
TCCAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

MALSSQIWAACLLLLLLASLTGSVFPQQTGQLAELOPQDRAGARASWMPMFQRRRRDTHFPI  
CIFCCGCCHRSKCGMCKT

**Important features:**

**Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 58-59

**N-myristoylation site.**

amino acids 44-50

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 1-12

## **FIGURE 45**

GTGGCTTCATTCAGTGGCTGACTTCCAGAGAGCAATTGGCTGGTCCCCAACATGCCTACCC  
TCATCTATATCCTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCTGAAAGAGCTGGTCGGT  
TCCGTTGGTGGGCCGTGACTTCCCCCTGAAGTCAAAGTAAAGCAAGTGACTCTATTGTCTG  
GACCTTCAACACAACCCCTCTTGTACCATACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA  
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAATGAAG  
AAGAATGACTCAGGGATCTACTATGTGGGATATAACAGCTCATCACTCCAGCAGCCCTCCACCCA  
GGAGTACGTGCTGCATGTCTACGAGCACCTGCTAAAGCTAAAGTCACCATGGGTCTGCAGAGCA  
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATT  
TATACCTGGAAGGCCCTGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC  
CTGGAGATGGGAGAAAGTGAATGACCTTCATCTGCCTGCCAGGAACCTGTCAGCAGAAACT  
TCTCAAGCCCCATCCTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCATG  
GTCCTCCTGTGTCTCCTGTTGGTCCCCCTCCTGCTCAGTCTCTTGACTGGGCTATTCTTG  
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGTGGACATTGTCGGG  
AAACTCTAACATATGCCCTCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT  
AGAACAAATCCTAAAGGAAGATCCAGCAAATACGGTTACTCCACTGTGGAAATACCGAAAAAGAT  
GGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTGCCTATGAGAATGTTA  
TCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCA

## **FIGURE 46**

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLSKVKQVDSIVWTFTNTPLVTIQP  
EGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK  
PKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIC  
VARNPVSRNFSSPIALKCEGAADDPDSSMVLLCLLIVPLLLSLEVLGLFLWFLKRERQEEYIE  
EKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT  
PRLFAYENVI

**Important features:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 224-250

**Leucine zipper pattern.**

amino acids 229-251

**N-glycosylation sites.**

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,  
291-295

## **FIGURE 47**

GGCTCGAGCGTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGG  
ATTCAGCCCTGCTGGTTCTACTGCTGTTAGGAGTAGTCTCAATGCCATACCCTCAATTGTCAGCT  
TAGTTGAGGAAGACCAATTTCCAAACCCCATCTCTGCTTGAGTGGTGGTCCCAGGAATT  
ATAGGAGCAGGTCTGATGCCATTCCAGCAACAACAATGTCCTGACAGCAAGAAAAAGAGCGTG  
CTGCAACAACAGAACTGGAATGTTCTTCATCATTTCAGTCAGTGTGATCACAGTCATTGGTGCTC  
TGTATTGCATGCTGATATCCATCCAGGCTCTCTAAAGGTCCCTCATGTGTAATTCTCCAAGC  
AACAGTAATGCCAATTGTGAATTTCATTGAAAAACATCAGTGACATTCCAGAATCCTCAA  
CTTGCAGTGGTTTCCAATGACTCTTGGCACCTCCTACTGGTTCAAAATAACCCACCAGTAACG  
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTCCACTTCGATTCTGAAGAAAACAAACATAGG  
CTTATCCACTTCTCAGTATTTAGGTCTATTGCTTGGAAATTCTGGAGGTCCTTGGCT  
CAGTCAGATAGTCATGGTTCTGGCTGTGTGGAGTCTTAAGCGAAGAAGTCAAATTG  
TGTAGTTAATGGGAAATAAAATGTAAGTATCAGTAGTTGAAAAA

## **FIGURE 48**

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA  
TTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNANCEFSL  
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHFSVFLGL  
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

**Important features:**

**Transmembrane domains:**

amino acids 10-31 (type II), 50-72, 87-110, 191-213

**N-glycosylation sites.**

amino acids 80-84, 132-136, 148-152, 163-167

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 223-227

**N-myristoylation sites.**

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 207-218

**TNFR/NGFR family cysteine-rich region protein.**

amino acids 4-12

## **FIGURE 49**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTGCCAAGGTGACCTCGCAGGACACTGGTGA  
AGGAGCAGTGAGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG  
ATCCGTGGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTCGAACTGTGA  
CATGGAGAGAGTGACCCCTGGCCCTCTCCTACTGGCAGGCCTGACTGCCTTGAAGCCAATGACC  
CATTTGCCAATAAGACGATCCCTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC  
TGCGGAGGGCTCTGGCCATTGCTGGGATCGCGGCAGTCTGAGTGGCAAATGCAAATACAAGAG  
CAGCCAGAACGAGCACAGTCCTGTACCTGAGAAGGCCATCCACTCATCACTCCAGGCTCTGCCA  
CTACTTGCTTGAGCACAGGACTGCCCTCCAGGGATGCCCTGAAGCCTAACACTGGCCCCCAGCACC  
TCCTCCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCT  
TTCTGATCAGGAGGCTTCTTATGAATTAAACTGCCACCACCCCTCA

## **FIGURE 50**

MERVTLALLLAGLTALLEANDPANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKS  
SQKQHSPVPEKAIPPLITPGSATTC

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 36-59

**N-myristoylation sites.**

amino acids 41-47, 45-51, 84-90

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.**

amino acids 54-67

## **FIGURE 51**

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG  
AGGACAGGGAGTCGGAAGGGAGGAGCACAGAGGAGGGCACAGAGACGCCAGAGCAAGGGCGCAAGG  
AGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGCAGAGTGAAGTCCAG  
GGGCCCTGGCCTGCCTCCTGCTGGCCCTCTGCTGGCAGTGGGAGGCTGGCCCTGAG  
CGGAGAGGAAAGCACTGGGACAATATTGGGAGGCCCTGGACATGGCCTGGAGACGCCCTGA  
GCGAAGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGAGCTGGCTCTAAAGTCAGTGAG  
GCCCTGGCCAAGGGACCAGAGAACAGCTGGCACTGGAGTCAGGCAGGTTCCAGGCTTGGCC  
AGCAGATGCTTGGCAACAGGGTCGGGAAGCAGGCCATGCTCTGGAAACACTGGGCACGAGA  
TTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCAGATGCTGTCCGGCTCTGGCAGGG  
GTGCCTGGCCACAGGGCTGGAAACTCTGGAGGCCATGGCATCTTGGCTCTCAAGGTGG  
CCTGGAGGCCAGGGCAAGGGCAATCCTGGAGGTCTGGGACTCCGTGGTCCACGGATAACCCG  
GAAACTCAGCAGGCAGCTTGGATGAATCCTCAGGGAGCTCCCTGGGTCAAGGAGGCAATGG  
GGGCCACCAAACCTGGGACCAACACTCAGGGAGCTGTGGCCCAGGCTGGCTATGGTTCAAGTGAG  
AGCCAGCAACCAGAATGAAGGGTGCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA  
ACTCTGGGGAGGCAGCGGCTCACAGTCGGCAGCAGTGGCAGTGGCAGCAATGGTACAACAAC  
AATGGCAGCAGCAGGGCTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAG  
TGGCGGAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGGAGGTGACAGCGGAGTGG  
CCTCCTGGGATCCAGCACGGCTCCTCCGGCAACCACGGTGGGAGCGGGAGGAAATGG  
CATAAACCCGGGTGTGAAAGCCAGGGATGAAGCCCGGGAGCGGGGAATCTGGGATTCAAGGG  
CTTCAGAGGACAGGGAGTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATGCCCTTG  
GAGGCTCTGGAGACAATTATGGGGCAAGGGTCAGCTGGGAGTGGAGGAGGTGACGCTGTT  
GGTGGAGTCATACTGTGAACTCTGAGACGTCCTGGGATGTTAACCTTGACACTTCTGGAA  
GAATTTAAATCCAAGCTGGTTCATCAACTGGGATGCCATAAACAAAGGACAGAGCTCTC  
GCATCCCGTGACCTCCAGACAAGGAGCCACAGATTGGATGGGAGCCCCCACACTCCCTCTTAA  
AACACCACCCCTCTCATCACTAACCTCAGCCCTTGGCCTTGAATAACCTTAGCTGCCCAACAAA  
AA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 52**

MKFQGPLACLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIKEAGGAAGSKVS  
EALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGPV  
GHSGAWETSGGHGIFGSQGGLGGQQGQGNPGGLGTPWVHYPGNSAGSFGMNPQGAPWGQGGNGGPPNF  
GTNTQGAVAQPGYGSVRASNQNEGCTNPPSGSGGGSSNSGGCGSQSGSSGSGSNGDNNNGSSGGS  
SSGSSSSGSSGGSSGGSSGSSGSGSRGDSGSESSWGSSTGSSGNHGGSGGGNGHPGCEKPGNE  
ARGSGESGIQGFRGQGVSSNMREISKEGNRLGGSGDNYRGQGSSWGSGGDAVGGVNTVNSETSPGM  
FNFDTFWKNFKSKLGFINWDAINKDQRSSRIP

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,  
90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,  
159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,  
236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,  
253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,  
283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,  
298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,  
325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,  
387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

## **FIGURE 53**

GGAGAAGAGGTTGTGTGGACAAGCTGCTCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG  
CTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGCTCCTGGCT  
ACTCGCCCGCATCCTGGCTTGGACCTATGCCCTCTATAACAACTGCCGCCGGCTCCAGTGTTC  
CACAGCCCCAAAACGGAACTGGTTTGGGTCACCTGGGCTGATCACTCCTACAGAGGAGGGC  
TTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCAGGGCTTACGGTATGGCTGGGCTCCAT  
CATCCCCTCATGTTTATGCCACCCCTGACACCACCGGTCTATCACCAATGCCCTAGCTGCCA  
TTGCACCCAAGGATAATCTTCATCAGGTTCTGAAGCCCTGGCTGGAGAAGGGATACTGCTG  
AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCGCCCTCCATTCAACATCCT  
GAAGTCCTATATAACGATCTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG  
CCTCAGAGGGCAGCAGTCGTCGGACATGTTGAGCACATCAGCCTCATGACCTGGACAGTCTA  
CAGAAATGCATCTTCAGCTTGACAGCATTGTCAGGAGAGGCCAGTGAATATATTGCCACCAT  
CTTGGAGCTCAGTGCCCTGTAGAGAAAAGGCCAGCATATCCTCCAGCACATGGACTTCTGT  
ATTACCTCTCCATGACGGGGCGCGCTTCCACAGGGCTGCCCTGGTGCATGACTCACAGAC  
GCTGTCATCCGGGAGCGGGCGTCGCACCCCTCCCCACTCAGGGTATTGATGATTTTCAAAGACAA  
AGCCAAGTCCAAGACTTGGATTCATTGATGTCCTGCTGAGCAAGGATGAAGATGGAAAG  
CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTCATGTTGGAGGCCATGACACCACG  
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCAGGGCACCCAGAAATACCAGGAGCGCTGCCG  
ACAGGAGGTGCAAGAGCTCTGAAGGACCGGATCTAAAGAGATTGAATGGACGACCTGGCC  
AGCTGCCCTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTACATCCCCAGCTCCCTCATC  
TCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGCCGAGTCATCCCCAAAGGCATTACCTG  
CCTCATCGATATTATAGGGGTCCATCACAAACCCACTGTCGGCCGGATCCTGAGGTCTACGACC  
CCTTCCGCTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTATTCTTTCTCCGCA  
GGGCCAGGAACTGCATGGGCAGGGCTTCGCCATGGGGAGATGAAAGTGGCCTGGCGTTGAT  
GCTGCTGCACTCCGGTCTGCCAGACCAACTGAGCCCCGCGAGGAAGCTGGAATTGATCATGC  
GCGCCGAGGGCGGGCTTGGCTGCCGGTGGAGCCCTGAATGTAGGCTTGCAGTGACTTCTGAC  
CCATCCACCTGTTTTGCAAGATTGTCATGAATAAAACGGTGCTGTCAAA

## **FIGURE 54**

MSLLSLPWLGRLPVAMSPWLLLLVVGSWLLARI LAW TYAFYNNCRLQCFPQPKRNWFWGHLG  
LITPTEEGLKDSTQMSATYSQGFTVWLGPPIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP  
WLGEGIILSGGDWKSRHRRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI  
SILMTLDLQLKCIFSFDSHCQERPEYIATILELSALVEKRSQHILQHMDFLYYLSDGRRFHRAC  
RLVHDFTDAVIRERRTLPTQGIDDFFKDKAKSKTLDFIGVLLSKDEDGKALSDEDIRAEADTF  
MFGGHDTTASGLSWVLYNLARHPEYQERCROEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR  
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPFVYDPFRFPENSKGRSP  
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN  
VGLQ

**Important features:**

**Transmembrane domains:**

amino acids 13-32 (type II), 77-102

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 461-471

**N-glycosylation sites.**

amino acids 112-116, 168-172

## **FIGURE 55**

ATCGCATCAATTGGGAGTACCATCTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTGA  
GCCTACTCGTTGATTGCAACTATCATGGTGTGTTGCACTTACCCGTGTTCTGCCT  
TTTGGTGCATAACAAGGGACTTGCACTTATCTCTGCATTTGCAGTCTTGGCATTGACGTGG  
TACAGCCTTCCATACCATTGCAAGGGATGCTGTGAAGAAGTGTGTTGCCGTGTCTTGC  
ATAATTCATGCCAGTTTATGAAGCTTGGAAAGGCACTATGGACAGAACGCTGGTGGACAGTTT  
GTAACTATCTCGAAACCTCTGTCTTACAGACATGTGCCTTTATCTTGCAGCAATGTGTTGCTT  
GTGATTCGAACATTGAGGGTTACTTTGGAAAGCAACAATACATTCTCGAACCTGAATGTCAGTA  
GCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAAATCTCCTCATGTACCTGTTCCTC  
TCTGGATGTTGTCCCACTGAATCCCCATGAATACAAACCTATTCAGCAACAGCAAAAAAAAAAAAAA  
AAA

## **FIGURE 56**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCASFWWHNKGLALIFCILQSLALTWYSLSFIPFAR  
DAVKKCFAVCLA

**Important features:**

**Signal peptide:**

amino acids 1-33

**Type II fibronectin collagen-binding domain protein.**

amino acids 30-72

**FIGURE 57**

CGGCTGAGCTCGAGCCGAATCGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCCGAAACATGCTCTGTGCGCTG  
TACGTGCCGTCATCGGGAGGCCAGACCGAGTTCAGACTTTGAGTCGAAGGGCTCCCTGCCAGTCAGTGAGTCC  
ATTTCAGACTCAGTGTCTCATCCCCCTCCAGGAATCTCCACCTACCCGCAGTGGAGACAGAAGAAATTCTACAAGCT  
GGAGATAAGGACCTTGTGGCGACTAGACTTGGAGAATTCTGTCATTATCTCAAGATCATGAGAAGAAGCTGAGG  
CTGGTGTAAAGTTGGACAAAAAGATGATGGAGCATTGACGCCAGGAGATCATGCACTCCGCCGGACTTC  
GGAGTCAGATATCTAACAGCAGGGCAGAAAAAAATTCTCAAGAGCATGGATAAAACGGCACGATGACCATCGACTGG  
AACGAGTGGAGAGACTACACCTCTCACCCCGTGGAAAACATCCCGAGATCATCTACTGGAGGATTCCACCG  
ATCTTGATGTGGTGGAGAATCTAACGGTCCCGATGAGTTCACAGTGGAGGAGAGCCAGACGGGGATGTGGTGAGA  
CACCTGGTGGCAGGGGGGGCAGGGGGCTATCCAGAACCTGCAAGGCCCTTGAGCAGGCTCAAGGTGCTCATG  
CAGGTGGCATGCCCTCCCACCAACATGGCATCTGGTGTCTACTCAGATGATTGCAAGAGGAGGGGCCAGG  
TCACCTGGGGGCAATGGCATCACGCTCTCAAATTGCCCCGAATCAGCCATCAAATTGCGCTATGAGCAG  
ATCAAGGCCCTGTGGTAGTGACCAGGAGACTCTGAGGATTACAGAGAGGCTGTGGCAGGGCTTGGCAGGGCC  
ATCGCCAGAGCAGCATCACCAATGGAGGCTCTGGAGAAGACCCGATGGCCTGCCAGAGCAGGCCAGTACTCAGGA  
ATGCTGGACTCGCGGAGGGAGACTCTGGCCAGAGGGGGTGGCCCTTCAACAAAGGCTATGCCCCAACATGCTG  
GGCATCATCCCCATGGCCATCAGCTTGCACTTGAGACCTCAAGAATGCCATCTGGCAGCAGCTACATGCTG  
AACAGCAGGGGACCCGGGGTGTCTGCTCTGGCCTGTGGCACCATGTCCAGTACCTGTGGCAGCTGGCAGCTAC  
CCCCCTGGCCCTAGTCAGGACCCGGATGCAAGGCCAACGCTCTATTGAGGGCCTCCGGAGGTGACCATGAGCAGCCTC  
TTCAAACATATCTGCGGACCGAGGGGGCTTGGGCTGTACAGGGGCTGCCCTTCAACATGAGGTGATGCCCA  
GCTGTGAGGATCAGCTACGTGGCTACAGAGAACCTGAGAATCACCTGGGCTGCACTGGCGTGACGGGGGGGG  
CGCCGGCACTGGACTCTGCTGAGCTCTGGGGCTGAGCCATCTGGGGTGTGAGCCACATCTACCTCTGTGAACTG  
AAGCTGTCTCGAGGCAACGATGTAACCCCTAGACGCCAGGGGGCTTGGGCTGAGGAGGCTGGCAGGGCTT  
GTCTCTGCTGACCCCAAGGACCTCTGGTTGTTCAAGGACAGGCTTCTGAGTGCCTGCAATAGTGAGCTTG  
CTCGGGCTCACATGTGTAAGGACAGGACATTCTGAGTGCCTGCAATAGTGAGCTTGAGGCTGGAGGCCGG  
TAGTTCTCCATTTCACCCCTGCAAGCAGCTTGGGACGGGCCCTGGGCTCTGGCTGCACTGGCGTGATCTCCCTGTG  
CCTCTTGCTGCCCTGCTCTGTGAGGTAAGGTTGGAGGGCTACAGGCCACATCCCCCTCTGGCTCAACTTCC  
ATAATCCATGATGAAAGGTGAGGTCAGCTGGGCTCCAGGCCCTGACTTCCCAACCTACAGCATTGAGCCTAAC  
TGGAGGAAAGAGGAAAGGATCTGGCCTTGTGCTCACTGCACTGAGCCCTGCTGATGGCTGGGCTCTCGGGCATG  
CTGGGAGTGCAGGGGGCTGGGCTGCTGGCTGCCAGAGGAAGGCAAGTGTGGGCTCATGGTGTCTGAGGCT  
GGCCTGGACCCCTGCAAGGATGGGCCAACCTCAGAACCAAACACTCTGTGCCCCACTGTGGCATGAGGGCACTGG  
CCATGTTGAGGGCAAGGGCAAGGCCCTGGGTTGTGTTCTGGGGAGGGCAAGGAAAGGTTGTGGAGGCCCTAATTATGG  
ACTGTTGGGAAAAGGGTTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
GAGCAGGAGCTGGCTGACTGCTCAAGAGTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
GGGACGAGCCCCACATTCCACTTGTGCACTGCTGGACACTTGTGTTATTGAGGAGGAGGAGGAGGAGGAGG  
AACTATTTTATAGATTGTTAATTAAATAGCTTGTCATTTCAACGTTATTTCATTTTATTTGAAACAGAGTTGCT  
GATTGCTACCTCCAAAGGCCGCCAGTGGGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
GTCCAGAGAAATTCTTGTGGGACTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
GTTGGGGAGGGCTTGGCCCTGGCCCTGGCTGAGGTTTGTGGGGCTGAGTGGGGCTGGAGAGAGGAGGAGGAGG  
AACCTTGAGGTTGAATTCAGTTAATTCTGCTGGGCTGGAGGGTTCTTATTTCATCTTGTGAAATGTCAGG  
TGAGGTGCCCTCACTGTGAAATTGTTGGTGGGGGGCTGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
CTTCTGCTGCCCTTGTGCTAACATGCGGCCACTGGCAGCTCACGGTGTCACTTCCATCCACAGGAATGACCTG  
TGAGGAAATTCTCAATAGGATGCAAGGATCAATGCAAAATTGTTATATGAAACATATAACTGGAGTCGTC  
CAAATTAGAAAGAATTGGAGCTTGAAGAGTTGTCATTAAAGCAGGCTTCAATAAAGTTGTTCAAGGCTGAAAAA  
AA

## **FIGURE 58**

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKDLDG  
QLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILKSMDKNG  
TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMWWRHLVAGGG  
AGAVSRTCTAPLDRLKVLMQHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIK  
FMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIAQSSIYPMEVLKTRMALRKTCQYSGMLDCARR  
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSADPGVFVLLACGTMSSTC  
GQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV  
VYENLKITLGVQSR

**Important features:**

**Signal peptide:**

amino acids 1-16

**Putative transmembrane domains:**

amino acids 284-304, 339-360, 376-394

**Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

**N-glycosylation sites.**

amino acids 129-133, 169-173

**Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

## **FIGURE 59**

GGAAGGCAGCGGAGCTCCACTCAGCCAGTACCCAGATA  
CGTGGAACCTTCCCCAGCCATGGC  
TTCCCTGGGGCAGATCCTCTTGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG  
CACTCATCATTGGCTTGGTATTCAGGGAGACACTCCATCACAGTCACTACTGTGCGCTCAGCT  
GGGAACATTGGGAGGATGGAATCCTGAGCTGCACTTGAACCTGACATCAAACTTCTGATAT  
CGTGATACAATGGCTGAAGGAAGGTGTTAGGCTTGGCCATGAGTTCAAAGAAGGCAAAGATG  
AGCTGTCGGAGCAGGATGAAATGTTAGGCTTGGCCATGAGTTCAAAGAAGGCAAAGATG  
GGCAATGCCCTTGGCTGAGGAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT  
CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAAACTGGAGCCTTCAGCATGCCG  
AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTGCGGTGTGAGGCTCCCCGATGGTCCCC  
CAGCCCACAGTGGCTGGCATTCCAAGTTGACCAAGGGAGCCACTCTCGGAAGTCTCCAAATAC  
CAGCTTGAGCTGAACCTTGAGAATGTGACCATGAAGGTTGTCTGTGCTACAATGTTACGA  
TCAACAAACACATACTCCTGTATGATTGAAAATGACATTGCCAAGCAACAGGGATATCAAAGTG  
ACAGAACATCGGAGATCAAAGGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTGTGT  
CTCTTCTTCTTGGCATCAGCTGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAATAAT  
GTGCCTGGCCACAAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTCAC  
CACCAGATATGACCTAGTTATATTCTGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG  
AGCAAACAAGAGCAAGAAACAAAAGCAGCAAGGCTCAATATGAACAAGATAAAAT  
CTATCTCAAAGACATATTAGAAGTTGGAAAATAATTGATGTGAACTAGACAAGTGTGTTAAGA  
GTGATAAGTAAATGCACGTGGAGACAAGTCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT  
CACCTGGGAGTGGAGGACAGGGATAGTGCATGTTCTGTGAAATTGTTATATGTG  
TGTAATGTTGCTCTGAGGAAGCCCTGGAAGTCATCCAAACATATCCACATCTTATATCCAC  
AAATTAAGCTGTAGTATGTACCTAACGCTGCTAAATGACTGCCACTCGCAACTCAGGGCG  
GCTGCATTTAGTAATGGGTCAAATGATTCACTTTATGATGCTCCAAAGGTGCCTGGCTTC  
TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTAGCATAAACAGAGCAGT  
CGGGGACACCGATTTATAAATAAACTGAGCACCTTCTTTAAACAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 6o**

MASLGQILFWSIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS  
DIVIQWLKEGVGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYKC  
YIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFPPQPTVVWASQVDQGANFSEVS  
NTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIKVTESEIKRRSHLQLLNSKASL  
CVSSFFAISWALLPLSPYIMLK

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 258-281

**N-glycosylation sites.**

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,  
220-224

**N-myristoylation sites.**

amino acids 52-58, 126-132, 188-194

## **FIGURE 61**

TGACGTCAAATCACCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG  
CACCAAGGAGCCCCCTCGGGTAGCTACTACCCCTGGACCCCCAATAGTGGAGGGCAGTATGGTAGT  
GGGCTACCCCCTGGTGGTTATGGGGGTCCTGCCCTGGAGGGCCTATGGACCACCAGCTGG  
TGGAGGGCCCTATGGACACCCCAATCCTGGATGTTCCCTCTGGA~~ACTCCAGGAGGACCATA~~TG  
GCGGTGCAGCTCCGGGGGCCCTATGGTCAGCCACCTCCAAGTTCCTACGGTGCCCAGCAGCCT  
GGGCTTATGGACAGGGTGGGCCCTCCCAATGTGGATCCTGAGGCCTACTCCTGGTCCAGTC  
GGTGGACTCAGATCACAGTGGCTATATCTCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA  
ATTGGTCTTCATTCAATGATGAGACCTGCCATGATGATAAACATGTTGACAAGACCAAGTCA  
GGCCGCATCGATGTCAGGCTCTCAGCCCTGTGAAATTCCAGCAGTGGAAAGAACCTT  
CCAGCAGTATGACCGGGACCGCTCGGGCTCATTAGCTACACAGAGCTGCAGCAAGCTCTGCCC  
AAATGGGCTACAACCTGAGCCCCAGTTACCCAGCTCTGGTCTCCCGCTACTGCCACGCTCT  
GCCAATCCTGCCATGCAGCTTGACCGCTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA  
GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGAAACATCCGGCTCAGCTTGAGGACTTCGTCA  
CCATGACAGCTTCTCGGATGCTTGACCCAAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT  
TCCTGGCTTCTTAGAGTGAGAGAAGTATGTTGACATCTCTTCTGTCCCTCTAGAAGAAC  
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCCTGCATCATGCCACCA  
AATAGTGAGGACCGGGGCTGAGGCCACACAGATAGGGGCTGATGGAGGAGAGGATAGAAGTTGA  
ATGTCCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCCAGGAGCAGGCTTGTAAATGG  
AGTTAGTGTCCAGTCAGCTGAGCTCCACCCCTGATGCCAGTGGTGAGTGTTCATGGCCTGTTACC  
GTTAGTACCTGTGTTCCCTCACCAAGGCCATCCTGTCAAACGAGCCATTTCCTCAAAGTGGAAAT  
CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAAGTGGCTGGATTCTGCCACACCCATAAAT  
CCTTGGTGTGTTAACCTCTAGCTGCCTGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGCAT  
CTTGCCAGGCTCTGCCCTGCAGCTGGACCCCTCACTGCCATGCTCTGCTCGGCT  
TCAGTCTCCAGGAGACAGTGGTACCTCTCCCTGCCAATACTTTTTAATTGCAATTTC  
ATTGGGCCAAAAGTCCAGTGAAATTGTAAGCTCAATAAAAGGATGAAACTCTGA

## **FIGURE 62**

MASYPYRQGCPGAAGQAPGAPPGSYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG  
HPNPGMFPSTPGGPYGGAAPGGPYGQPPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDSDH  
SGYISMKELQALVNCNWSSFNDETCLMMINMFDTKSGRIDVYGFSAWKFIQQWKNLFQQYDR  
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQLTEAFREK  
DTAVQGNIRLSFEDFVTMTASRML

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-  
66, 70-75, 78-83, 83-88, 87-92, 110-115

### **FIGURE 63**

CAGGATGCAGGGCCCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATC  
TCCCAGGCCTTTGCCGGAGCATCGGTGTTGGAGGAGAAAGTTCCAAAACTTCGGGACC  
AACTTGCCCTCAGCTCGGACAACCTCCTCCACTGGCCCTCTAAGCTGAACATCCGCAGCCGC  
TCTGGACCCTAGGTCTAATGACTTGGCAAGGGTCTCTGAAGCTCAGCGTGCCTCCATCAGATG  
GCTTCCCACCTGCAGGAGGTTCTGCAGTGCAAGAGGTGGCCTCCATCGTGGGGCTGCCTGCCATG  
GATTCCCTGGCCCCCTGAGGATCCTGGCAGATGATGGCTGCTGCGGCTGAGGACCGCCTGGGGGA  
AGCGCTGCCCTGAAGAACTCTTACCTCTCAGTGCTGCCGGCCCTCGCTCCGGGAGTGGCCCTT  
TGCCTGGGAGTCTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGAC  
TCGGAGTCCAGACGACTGCCCGTTCTAATTCACTGGGAGCCGGGGAAAAATCCTTCCAAACG  
CCCTCCCTGGTCTCATCCACAGGGTCTGCCTGATCACCCCTGGGTACCTGAATCCAGTG  
TGTCCCTGGGAGGTTGGAGGCCCTGGACTGGTGGGAACGAGGCCATGCCACACCCCTGAGGGA  
ATCTGGGTATCAATAATCAACCCCCAGGTACCAAGCTGGGAAATATTAATCGGTATCCAGGAGG  
CAGCTGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGAAATATTAATCGGTATCCAGGAG  
GCAGCTGGGAAATATTCACTATACCCAGGTATCAATAACCCATTCCCTGGAGTTCTCCGC  
CCTCCTGGCTTCTGGAACATCCCAGCTGGCTCCCTAATCCTCCAAGCCCTAGGTTGCAGTG  
GGGCAGAGCACGATAGAGGGAAACCCAACATTGGGAGTTAGAGTCCTGCTCCGCCCTGCTG  
TGTGGGCTCAATCCAGGCCCTGTTAACATGTTCCAGCACTATCCCCACTTTCAAGTGCCTCCCC  
TGCTCATCTCCAATAAAATAAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA

## **FIGURE 64**

MQGRVAGSCAPLGLLLVCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGPSNSEHPOPAL  
DPRSNDLARVPLKLSVPPSDGFPPAGGSAVQRWPPSWGLPAMDSWPPEDPWQMMAAAEDRLGEA  
LPEEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRLPRSNSLGAGGKILSQRP  
PWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWGTRPMFHPEGIWGGINNQPPGTSGNINRYPGGS  
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPGVLRPPGSSWNIPAGFPNPPSPRLQWG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Casein kinase II phosphorylation sites.**

amino acids 56-59, 155-158

**N-myristoylation sites.**

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,  
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

## **FIGURE 65**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTTGGGTGCTGGGCTGCCCTTGCTCCTCTTGACCCCTGGCAGCTCACATGGAACAGGGCCGGGTATGA  
CTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCCTCATGAGTCCAGCTCCTGGAA  
TTGCTTAAAAGCTCTGCCTCCTCCATCTCCCTCAGGGACCAGCGTCACCCCTCACCATGC  
AAGATCTAACACCATGTTGTCTGCAACACATGACAGCCATTGAAGCCTGTGTCTTCTTGGCCC  
GGGCTTTGGGCGGGGATGCAGGAGGCAGGCCCGACCCGTCTTCAGCAGGCCACCCCTC  
CTGAGTGGCAATAAATAAAATTGGTATGCTG

## **FIGURE 66**

MGSGLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSTSVTL  
HHARSQHHVVCNT

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 37-41

**N-myristoylation sites.**

amino acids 15-21, 19-25, 60-66

## **FIGURE 67**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCGGGC  
CAGGTGCCCGTCGCAGGTGCCCTGGCCGGAGATGCGGTAGGAGGGCGAGCGCGAGAACCCCC  
TTCCTCGCGCTGCCAACCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGCTGCTCTGGCG  
CTGGGCTGCCGTTCCCTGCTGGCCCGCTGGGGCGAGCCTGGGGCAAATAACAGACCAACTCTGC  
AAATGAGAATAGCACTGTTGCCCTCATCCACCAGCTCCAGCTCCAGTGGCAACCTGCGTCCGG  
AAGCCATCACTGCTATCATCGTGGCTTCTCCCTTGGCTGCCTTGCTCCTGGCTGTGGCTG  
GCACTGTTGGTGCAGGCTTCGGAGAACGGCAGACGGAGGGCACCTACCGGCCAGTAGCGA  
GGAGCAGTTCTCCATGCAGCCGAGGCCGGCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT  
GCCTGCCATCTAGGTCCCTCTGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGAAGAAGGTACTCAA  
GGCAGTGCCCTCTGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGAAGAAGGTACTCAA  
AGACTCTGCCCTGAGGTCAAGAGAGGATGGGCTATTCACTTTATATTTATATAAAAATTAG  
TAGTGAGATGTAAAAAAAAAAAAAA

## **FIGURE 68**

MANPGLLLLALGLPFLARWGRAWGQIQTTSANENSTVLPSSSSDGTLRPEAITAIIVVFS  
LLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFShAAEARAPQDSKETVQGCLPI

**Important features:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 56-80

**N-glycosylation site.**

amino acids 36-40

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 86-90

**Tyrosine kinase phosphorylation site.**

amino acids 86-94

**N-myristoylation sites.**

amino acids 7-13, 26-32

## **FIGURE 69**

## FIGURE 70

MGLFRGFVFLLVLCLLHQSNNTSFIKLNNNGFEDIVIVIDPSVPEDEKIEQIEDMVTTASTYLFE  
ATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGHEY  
IHFTPDLGGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCAGISGRN  
RKYKCQGGSCLSRACRIDSTTKLYGKDCQFPDKVQTEKASIMFMQSIDSVVEFCNEKTHNQEAP  
SLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLVLDKSGSMGGKDRLNR  
MNQAAKHFLQLTVENGSSWVGMVHFSTATIVNKLIQIKSSDERNTILMAGLPTYPLGGTSICSGIK  
YAFQVIGELHSQDGSEVLLTDGEDNTASSCIDEVKQSGAIVHFTIALGRAADEAVIEMSKITGG  
SHFYVSDEAQNNGLIDAEGALTSGNTDLSQKSLQLESKGLTLSNAWMNDTVIIDSTVGKDTFFL  
ITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR  
AANSSVPPITVNAKMNDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNA  
GADSFKNQDGYSRYFTAYTENGRYSLKVRAGGANTARLKLRRPLNRAAYIPGWVNGEIEANPP  
RPEIDEDTQTTLDFSRTASGGAFVVSQVPSLPLPDQYPPSQITDLDATVHEDKIIILTWTAPGDN  
FDVGVKVQRYIIRISASILDLRDSFDDALQVNNTDLSPKEANSKESFAFKPENISEENATHIFIAI  
KSIDKSNLTSKVSNTAQVTLFIPQANPDDIDPTPTPTPTPKSHNSGVNISTLVLSIGSVVI  
VNFILESTTI

**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

## FIGURE 71

CTCCCTAGGTGGAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGAAAGACCATACTGCCCGGGCAGGGTGA  
CAACAGGTGTCATTTTGATCTCGTGTGGCTGCCCTATTCAAGGAAAGACGCCAAGGTAACTTGACCCA  
GAGGAGCAATGATGTAAGCACCCTCTAACCTTCCCTTCTGAAACCCAGTTATGCCAGGATTTACTAGAGGTGTC  
ACTCAACCAGCAAGCGCTCTCGCTTAACTTGTTGGAGGAGAAACCTTGTGGGGCTGCCTCTTAGCA  
GTGCTCAGAAGTACTGCTGAGGGTGGACAGAAGAAAGGAAAGGCTCCCTTGCTGTTGGCTGCACATCAGGAA  
GGCTGTGATGGGAATGAAGGTGAAACTTGAGATTCACTCAGTCATTGCTCTGCCCTGCAAGATCATCCTTAAA  
AGTAGAGAAAGCTGTCGTGTGGTGGTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAGCAGCTC  
CGGGGGCCCCAACCGCATCTCCCTGTGGTAGGCCAGGGAAAGCCCTTCTGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
ACCGGTTCTGGACGATGGCTGATTCTGATGATGGTGGCTGCCGGGGCTGCTGCTGGGATTTCCCGGGGGGG  
GTTTGTGCTGGCTCTCTGCTGCTATCTCTGCTCTGATCTGTCCTGACAGTGGCCCTGCACCCCAAAGGTTGACGAGGAGCAG  
CTGGCACTGCCAGGGCAACAGCCCCACGGGGAAAGGAGGGTACCAAGGCCCTCAGGAGTGGGGAGGAGCAC  
CGCAACTACGTGACGCCAGCAGTCAGGCCAGCTCAAGGAGGAGCTGCCAGGAGAGGAGTGAGCAGCTCAGG  
AATGGGAGTACCAAGGCCAGCAGTCAGTGTGGCTGCCCTGGCTGGACAGGAGCCCTCCAGGAGAAAACCCAGGCCAGCTC  
CTGGCCTCTGACTCGCAGGGTGGACAGGAGAGGAGTGAAGTGTGGCTCAAGCTGGCCACAGAGTATGCAAGCAGTG  
CCTTCGAGTAGCTTACTCTACAGAAGGTGACCTGGAGACTGGCTTACCCGCCACCCGAGGAGAACCTGCTG  
AGGAAGGACAAGCGGGATGAGTTGGTGAAGCATTGAACTCAGCCTGGAGACCCATGCAACAATCTGCAAGAACAGC  
CCCAATCACCGTCTTACAGGCCCTGATTCTAGAAGGGATCTACCGAACAGAAAGGGACAAGGGACATTGAT  
GAGCTCACCTTAAAGGGGACCAACACGAACTTACCGCTCATCTTATTCTGACCATTCAGGCCCATCATGAAA  
GTGAAAAATGAAAGCTAACATGGCAACACGCTTACATGTATCTGCTCTAGCAAAAAGGGTGGACAAGTTC  
CGCGAGTTCATGCAAGATTTCAAGGGAGATGCAATTGAGCAGGATGGAGAGTCCATCTCACTGTGTTTACTTGGG  
AAAGAAGAAATAATGAAGTCAAAGGAATACTTGAAACACTTCAAAAGCTGCCAACTTCAGGAATTCTCATC  
CAGCTGAATGGAAATTCTGGGAAAGGGACTGATGTTGGAGCCGCTTCTGGAAGGGAAACGCTCTTCTC  
TTTTCTGTGATGPGACATCTACTTACATCTGAATTCTCAATACGTTGAGGCTGAATACACAGCCAGGGAAAG  
GTATTCTGAGTCTGCTTCACTGCAAGTACAATCTGCTGATGACGTTCTCCCTGGAA  
CAGCAGCTGGTCAAAAGAAGGAATGGATTGGAGAGACTTGGATTGGGATGACCTGTCAGTATCGTCAGAC  
TTCATCAATATAGTGGGTTGATCTGGACATCAAAGGCTGGGGGGAGAGGATGTCACCTTATCGCAAGTATCTC  
CACAGAACCTCATAGTGTACGGACGCCCTGCGAGGACTCTCCACCTCTGGCATGAGAACGGCTGCTGGACGAG  
CTGACCCCGAGCAGTACAAGATGTGCACTGCAAGGCTAACAGGCTACCCACGGCCAGCTGGGCTGCTG  
GTGTTCAAGCAGGAGATAGGGCTACCTTCCGAAACAGAAAGACAAGTAGCAAAAACATGAACTCCAGA  
GAAGGATTGTGGGAGACACTTTTCTTCTTGTCAATTACTGAAAGTGGCTCAACAGAGAAAGACTTCA  
GGACGACAAAAGAATTGGACTGATGGGTAGAGATGAGAAAGCCTCGATTCTCTGTTGGGTTTACACAGA  
AATCAACAAATCTCCCTTGCCTGAAAGTAACCCATTGCAAGTCTGCAAAAGGCAGAAATGCTG  
AGATTATAAGGCTTAAGGTGGAGGTTTGATGGTTTACAATACACTGAGAGTCTGTTGGCTCATGAA  
AATATCATGATTAAAGACGAGTTGGTAAAGGATTTCTGAGATGCAATTGAGACATTTCTCTCATATGAATGA  
GCCTATCAGCAGGGCTAGTTCTAGGAATGCTAAATATCAGAAGGAGGGAGAGGAGATAGGTTATTATGAACT  
AGTGAGTACATTAAGTAAATAATGGACAGAAAGAAAGAACCTAAATATCGTGTCAATTCTCCCAAGAT  
TAACCAAAATCTGTTATCTTTGGTTGCTTTAACTGTCCTGTTTCTTCTTATTAAAGGACT  
TTTTCTCTGAGTTAGTCTGCTTATTTAACTTACCTGTCAGGCTTACAAGAGAGCACAAGTGGCTAC  
ATTTTTATTTTAAAGGAGATTTCTGAGATGCAATTGAGACATTCTCAGTCAAGCATCAATTGATGCCATAT  
CCAAGGACATGCCAAATGCTGATTCTGCAAGGACTGAATGTCAGGCATTGAGACATAGGGAGGAATGGTTGACT  
AATACAGACGTACAGATACTTCTGTAAGAGTATTGCAAGAGGAGCAACTGACACTGGAGGAAAGAAAATGAC  
ACTTTCTCTTACAGAAAAGGAAACCTCATTCAGACTGGTATCTGCTGACTAAAGTCAGAACCCACATT  
CTCCTCAGAAGTAGGGACCGCTTCTTACCTGTTAAATAACCAAGTATACCGTGTGAACCCAACATCTTTC  
AAAACAGGGTGCCTCTGCTTGGCTTCCATAAGAAGAAATGGAGAAAATATATATATATATATATATG  
GAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTGCTACATGTTATCCACCCAGGGCCAGGTGGAAG  
TAAGTGAATTATTTTAAATTAAAGCAGTTACTCAATCAGCAAGATGCTCTGAAAATTGCAATTG  
CAAACATTTTAAATAATACAGTTAACATAGTGGTTCTCATTGATGAAAATTATAGCCAGCACCAG  
ATGCACTGAGCTAATTATCTCTTGTGAGCTCTGCTTGTCAAGTAAACTCATTGTTAAAGCTTCAAGAAC  
ATTCAAGCTGTTGGTGTGTTAAAGGATGCAAGTGTGTTGATTGACTGGTAGTTGATGAAATTAAATTAAACACAGG  
CCATGAATGGAAGGTGGTATTGCAAGCTAATAAAATGATTGTGGATGAA

## FIGURE 72

MMVRGLLAWISRVVVLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEWE  
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDK  
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVRKDKRDELVEAIESALETLNNPA  
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVNEKLNMAN  
TLINIVPLAKRVDKFQFMQNPREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNF  
TFIQIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFQSQY  
NPGIIYGHDAVPPLEQQLVIKKETGFWRDFGFGMTQCQRSDFINIGGFDDIKGWGGEDVHLYR  
KYLHSNLIVVRTPVRLFHLWHEKRCMDELTPHQYKCMQSKAMNEASHGQLGMLVFRHEIEAHL  
RKQKQKTSSKKT

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 315-319, 324-328

**N-myristoylation sites.**

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

**Amidation site.**

amino acids 377-381

### FIGURE 73

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGAGTTGCTCTGGGATCCA  
GAAACCCATGATAACCTACTGAACACCGAATCCCCTGGAAGGCCACAGAGACAGAGACAGCAAGA  
GAAGCAGAGATAAAACACTCACGCCAGGGCTCGCTCGCTCTCTCTCTCTCACTCCTC  
CCTCCCCCTCTCTCTGCTCTAGTCCTCTAGTCCTCAAATTCCAGTCCCCCTGCACCCCTTC  
CTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTGGATCCTGGCTGCAGATGGG  
GTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCAGCCTTACCCGTAGTGT  
GGAAACAATGCCAGTGCCTCATCGATATTGACAGACAGTGTGACATTGACCTGATTGCC  
TGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTGGACCTGCACAACAATGCC  
ACACAGTGCAACTCTCTGCCCTCACCCGTATCTGGTGGACTTCCCCGAAAATATGTAGCT  
GCCAGCTCCACCTGCACTGGGTAGAAAGGATCCCCAGGGGGTCAAGAACACCAGATCAACAG  
TGAAGCCACATTGCAAGAGCTCACATTGTACATTATGACTCTGATTCTATGACAGCTTGAGTG  
AGGCTGCTGAGAGGCCAGGGCTGGCTGCTGGCATCCTAATTGAGGTGGGTGAGACTAAG  
AATATAGCTTATGAAACACATTGAGTCACTTGCACTGAAGTCAGGCATAAAGATCAGAACACTC  
AGTGCCCTCCCTCAACCTAACAGAGAGCTGCTCCCCAACAGCTGGGCAGTACTCCGCTACAATG  
GCTCGCTCACAACTCCCCCTGCTACCAAGAGGTGCTGGACAGTTTTATAGAAGGTCCAG  
ATTTCAATGAAACAGCTGGAAAGCTTCAGGGACATTGTTCTCCACAGAACAGGCCCTCTAA  
GCTTCTGGTACAGAAACTACCGAGCCCTCAGCCTCTCAATCAGCGCATGGCTTGCTTCTTCA  
TCCAAGCAGGATCCTCGTATACCACAGGTGAAATGCTGACTTAGGTGAGGAATCTGGTTGGC  
TGTCTGCTCTCTGGCTTTATTCATTGCTAGAAAGATTGGAAGAACAGGGCTGGAAAA  
CCGAAAGAGTGTGGCTTCACCTCAGCACAAAGCCACGACTGAGGCATAAATTCTCTCAGATAC  
CATGGATGTGGATGACTTCCCTCATGCCATCAGGAAGCCTCTAAATGGGGTAGGATCTGG  
CCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCCTGGACATCTTAGAGAGGAAT  
GGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTCAGCCTCTCCAAACATGTAGGAGGAA  
ATGAGGAAATCGCTGTGTTAATGCAGAGANAAACTCTGTTAGTTGCAGGGGAAGTTGGG  
ATATACCCCAAAGTCCCTCACCCCTCACTTTATGCCCTTCCCTAGATATACTGCGGGATCT  
CTCCTTAGGATAAAGAGTTGCTGTGAAGTTGATATTTGATCAATATATTGGAAATTAAAG  
TTTCTGACTTT

## FIGURE 74

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFPDLPALQ  
PHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEAT  
FAELHIVHYDSDSYDSLSEAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP  
FNLRELLPKQLGQYFRYNGSLTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLV  
ONYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS  
VVFTSAQATTEA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

## **FIGURE 75**

TGCCGCTGCCGCCGTGCTGCTGGCTCTGGCGGCCCTGGGACGGGCAGTCCCTGTGTC  
TCTGGTGGTTGCCTAACCTGCAAACATCACCTTATCCATCAACATGAAGAATGTCCCTACA  
ATGGACTCCACCAGAGGGCTTCAAGGAGTTAAAGTTACTACACTGTGCAGTATTCACTACAA  
ATTGGGCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTGTCCTGACAGCTCC  
AGAGAAGTGGAAAGAGAAAATCCAGAAGACCTCCTGTTCCATGCAACAAATATACTCCAATCTGA  
AGTATAACGTGTCTGTGTTGAATACTAAACAGAACGTGGTCCCAGTGTGACCAACCAC  
ACGCTGGTGCTCACCTGGCTGGAGCGAACACTCTTACTCGTACACGTGGAGTCCTCGTCCC  
AGGGCCCCCTCGCCGTGCTAGCCTTCTGAGAAGCAGTGTGCCAGGACTTGAAAGATCAATCAT  
CAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTGCCATATCTATTACCGTGTCTTTT  
TCTGTGATGGCTATTCCATCTACCGATATCCACGTGGCAAAGAGAAACACCCAGCAAATT  
GATTTGATTTATGAAATGAATTGACAAAAGATTCTTGTGCCGTGAAAAATCGTGATTA  
ACTTTATCACCTCAATATCTGGATGATTCTAAATTCTCATCAGGATATGAGTTACTGGGA  
AAAAGCAGTGTATCCAGCCTTAATGATCCTCAGCCAGCGGGAACCTGAGGCCCCCTCAGGA  
GGAAGAGGAGGTGAAACATTAGGGTATGCTCGCATTGATGAAATTGGACTCTGAAG  
AAAACACGGAAGGTACTCTCTCACCCAGCAAGACTCCCTCAGCAGAACAAATACCCCCGGATAAA  
ACAGTCATTGAATATGAATATGATGTCAGAACCACTGACATTGTGCCGGGCTGAAGAGCAGGA  
GCTCAGTTGCAGGAGGGTGTCCACACAAGGAACATTGGAGTCGCAGGCAGCGTGGCAG  
TCTTGGCCCCGAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCG  
CAGGAGCACACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCCTGGTCAGTGGGA  
TCCCCAAACTGGCAGGCTGTGTATTCCCTCGCTGTCCAGCTCGACCAGGATTAGAGGCTGCG  
AGCCTCTGAGGGGATGGCTCGGAGAGGGCTTCTATCTAGACTCTATGAGGAGCCGGCT  
CCAGACAGGCCACCAAGGAGAAAATGAAACCTATCTCATGCAATTGAGGAATGGGGTTATA  
TGTGAGATGGAAAACTGTGCCAACACTTCCTTGCCTTGTGACTTGTGAG  
TCACCCCTTGATCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTCCAGTTGTGAAACAGTGA  
CTGTGAGAATTACTTATTCTTCTATTCTCATAGCACGTGTGATTGGTCATGAGTGA  
GGTCTCTTAACAATGATGGTGGCCTCTGGAGTCAGGGCTGGCGTTGTTATGCAGAGAA  
AGCAGTCAATAATGTTGCCAGACTGGGTGCAGAATTATTAGGTGGGTGT

## **FIGURE 76**

MSYNGLHQRFKELKLLTLCISISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIY  
SNLKYNVSLNTKSNRTWSQCVTNHTLVLWLEPNTLYCVHVESFVPGPPRRAQPSEKQCARTLK  
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGYNEFDKRFVPAEK  
IVINFITLNISDDSKISHQDMSSLGKSSDVSSLNDPQPSGNLRPPQEEEVVKHLGYASHLMEIFC  
DSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQELSLOEEVSTQGTLLSQA  
ALAVLGQTLQYSYTPQLQDLDPLAQEHTDSEEGPEEPSTTLVDWDPQTGRLCIPSLSSFDQDS  
EGCEPSEG DGLGEEGLLSRLYEEPAPDRPPGENETYLMQFMEEWGLYVQMN

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

## FIGURE 77

GAGGAGGGGCCGAGGACTCCAGCGTCCCCAGGTCTGGCATCCTGCACCTGCTGCCCTCTGACAC  
CTGGGAAGATGGCCGCCGTGGACCTTCACCCCTCTCTGTGGTTGCTGGCAGCCACCTTGATC  
CAAGCCACCCCTCAGTCCCCTCAGTCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC  
ACAGGGAGCTGAAGGACCACAACGCCACCAGCATTCTGCAGCAGCTGCCGTGCTCAGTGCATGC  
GGGAAAAGCCAGGCCGGAGGCATCCCTGTGCTGGCAGCCTGGTGAACACCCTGAAGCACATC  
ATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTGCCAATGACCA  
GGAGCTGCTAGTCAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTGGTCAAGACCA  
TCGTGGAGTTCCACATGACGACTGAGGCCAAGCCACCATCCGCATGGACACCAGTGCAGTGGC  
CCCACCCGCTGGCTCAGTGACTGCCACCAGCCATGGGAGCCTGCGCATCCAACTGCTGTA  
TAAGCTCTCCTTCCTGGTGAACGCCCTAGCTAACGCAGGTCTAGTGGCCATGCCCTGGTCA  
CCAATCTAGTGAAAAACCAGCTGTGCTCCGTGATCGAGGCTTCCCTCAATGGCATGTATGCAGAC  
CTCCTGCAGCTGGTGAAGGTGCCATTCCCTCAGCATTGACCGTCTGGAGTTGACCTTCTGTA  
TCCTGCCATCAAGGGTACACCATTAGCTCACCTGGGGCCAAGTTGGACTCACAGGGAA  
AGGTGACCAAGTGGTCAATAACTCTGCAGCTCCCTGACAATGCCACCCTGGACAACATCCCC  
TTCAGCCCTCATCGTGAGTCAGGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCCAGAAGA  
ATTCATGGTCTGGACTCTGTGCTTCCCTGAGAGTGCCCCATGGCTGAAGTCAGCATGGG  
TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTAAGAGTCTTCAACTCAGGAC  
ACTCCCGAGTTTTATAGACCAAGGCCATGCCAAGGTGCCCAACTGATCGTGCTGGAGTGT  
TCCCTCCAGTGAAGGCCCTCCGCCCTTGTCACCCCTGGGATCGAAGGCCAGCTCGGAAGCTCAGT  
TTTACACCAAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATGGATCCAGCTG  
ATGAACTCTGGGATTGGCTGGTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA  
CTCCATCCTGCTGCCGAACCAGAACGAATTAAGATCTGGGTCCAGTGTCATGGTGAAGG  
CCTTGGGATTCGAGGCCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGCTTACTCCAGCCTC  
TTGTGGAAACCCACAGCTCTCTGTCTCCCAGTAAGACTTGGATGGCAGCCATCAGGGAAGGTG  
GTCCCAGCTGGGAGTATGGGTGTGAGCTCTAGACCATCCCTCTGCAATCAAAAAACTTG  
CCTGTGAAAAAA

## **FIGURE 78**

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPVKIKEKLTQELKDHNATSILQQLPLLSAMREK  
PAGGIPLVGLSLVNTVLKHIIWLKVITANIQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE  
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSIRIQLLYKLSFLVNALAKQVMNLLVPSLPNL  
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYLGAKLDSQGKVT  
KWFNNSAASLTMPPTLDNIPFSLIVSQDVVKAAVAAVLSPPEEFMVLLDSVLPEAHRLKSSIGLIN  
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSEALRPLFTLGIEASSEAQFYT  
KGDQLILNLNNISSLRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNONGKLRSGVPVSLVKALG  
FEAAESSLTKDALVLTPASLWKPSSPVSQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

## FIGURE 79

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC  
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGTTCTACTGAGAGGTCTGCCATGGCCTCT  
CTTGGCCTCCAACTTGGGGCTACATCCTAGGCCTCTGGGCTTTGGGCACACTGGTGCCAT  
GCTGCTCCCCAGCTGGAAAACAAGTTCTATGCGGTGCCAGCATTGTGACAGCAGTTGGCTCT  
CCAAGGGCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGC  
ACCCTCTGGGCTGCCGCTGACATCCAGGCTGCCAGGCCATGATGGTGACATCCAGTGCAAT  
CTCCTCCCTGGCCTGCATTATCTGTGGCATGAGATGCACAGTCTCTGCCAGGAATCCC  
GAGCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTCATCCTGGAGGCCTCCTGGGATTC  
ATTCCCTGTTGCCTGGAATCTCATGGGATCCTACGGGACTCTACTCACCACTGGTGCCTGACAG  
CATGAAATTGAGATTGGAGAGGCTCTTACTGGGATTATTCTCCCTGTTCTCCCTGATAG  
CTGGAATCATCCTCTGCTTTCTGCTCATCCCAGAGAAATCGCTCCAACTACTACGATGCCTAC  
CAAGCCAACCTCTGCCACAAGGAGCTCCAAGGCCTGGTCAACCTCCAAAGTCAGAGTGA  
GTTCAATTCCTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGCCAGAGCTGGGGGTGGCTG  
GGTCTGTAAAAACAGTGGACAGCACCCCGAGGCCACAGGTGAGGGACACTACCAACTGGATCGT  
GTCAGAAGGTGCTGCTGAGGATAACTGACTTTGGCATTGGATTGAGCAAAGGCAGAAATGGGG  
GCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTGCCATGCCAGCTTCTGTTCC  
TCACCTGCTGCCCTGCCCTAACCTCAACTGAAACCCATTCCCTTAAGCCA  
GGACTCAGAGGATCCCTTGCCTCTGGTTACCTGGACTCCATCCCAAACCCACTAATCACA  
TCCCACTGACTGACCCCTGTGATCAAAGACCCCTCTGGCTGAGGTTGGCTTAGCTCATT  
GCTGGGATGGAGAGGAGAAGCAGTGGCTTGTGGCATTGCTCTAACCTACTCTCAAGCTTC  
CCTCCAAAGAAACTGATTGCCCTGGAACCTCCACTCTGTTATGACTCACAGTGTCCA  
GACTAATTGTCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG  
CAGGATGGGAGGACAGGAAGGCAGCCTGGACATTAAAAAAATA

## **FIGURE 8o**

MASLGLQLVGYILGLLGLLGTIVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD  
IYSTLLGLPADIQAAQAMMVTSIASSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL  
LGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGISSLFSLIAGIILCFSCSSQRNRSNYY  
DAYQAQPLATRSSPRPGQPPKVKEFNSYSLTGYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

## **FIGURE 81**

CCACCGCGTCCGCCTCTCCCTCTGCTGGACCTTCCTCGTCTCCATCTCCTCCCTTT  
CCCGCGTTCTCTTCCACCTTCTCTTCCACCTTAGACCTCCCTGCCCTCCTTCC  
GCCCACCGCTGCTTCCCTGGCCCTCTCGACCCGCTAGCAGCACCTCTGGGTCTGTGG  
GTTGATCTGTGGCCCTGTGCCCTCGTCTTCTGCTCCCTCTCCGACTCCGCTCCCG  
ACCAGCGGCTGACCTGGGAAAGGATGGTCCCGAGGTGAGGGTCTCTCCCTTGCTGGGA  
CTCGCGTCTGGTCCCCCTGGACTCCACGCTGAGCCGCCAGACATGTTCTGCCTTT  
CCATGGGAAGAGATACTCCCCCGAGAGCTGGCACCCCTACTGGAGCCACAAGGCTGATGT  
ACTGCCCTGCGCTGTACCTGCTCAGAGGGGCCATGTGAGTTACCGCCTCACTGTCCGCC  
GTCCACTGCCCTGACGGAGCCACAGCAATGCTGTCCAAGTGTGTGGAACCTCACAC  
TCCCTCTGGACTCCGGCCCCACCAAAGTCCCTGCCAGCACAAACGGGACCATGTACCAACACGGAG  
AGATCTCAGTGCCCATGAGCTGTTCCCCTCCGCCACTGGAGCCACAAGTGTGTCTGCAGCTGC  
ACAGAGGGCCAGATCTACTGCCCTCACAAACCTGCCCGAACCGAGGCTGCCAGCACCCCTCCC  
ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACA  
GTGTGCAGTCGCTCCATGGGTGAGACATCCTCAGGATCCATGTTCCAGTGTGCTGGAGAAAG  
AGAGGCCGGCACCCAGCCCCACTGGCCTAGCGCCCTCTGAGCTTCCATCCCCTGCCACTT  
CAGACCCAAGGGAGCAGGCAGCACAACTGTCAGATCGCTGAAGGAGAAACATAAGAAAGCCT  
GTGTGCATGGCGGGAAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCTTCCGTGCCCTCGC  
CCCTTCCCCTGCATCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC  
CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCCAGAGG  
ACAAAGCAGACCCCTGCCACAGTGAGATCAGTCTACCAGGTGTCCAAGGCACCGGGCCGGTC  
CTCGTCCACACATCGGTATCCCCAGCCAGACAACCTGCGTCGCTTGCCCTGGAACACGAGGC  
CTCGGACTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAAACTGAGGCTCAGAGAG  
GTGAAGTACCTGGCCAAGGCCACACAGCCAGAATCTTCACTTGACTCAGATCAAGAAAGTCAG  
GAAGCAAGACTCCAGAAAGAGGCACAGCACTCCGACTGCTCGCTGGCCCCACGAAGGTCACT  
GGAACGTCTCCTAGCCCAGACCCCTGGAGCTGAAGGTACGCCAGTCCAGACAAAGTGACCAAG  
ACATAACAAAGACCTTAACAGTTGAGATATGAGCTGTATAATTGTTATTATATTTAATAAA  
TAAGAAAGTTGCATTACCCCTCAAAAAAAAAAAAAAA

## **FIGURE 82**

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSE  
GAHVSCYRLHCPPVHCPQPVTPEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELP  
PSRLPNQCVLCSCTEGQIYCGLTCPEPGCPAFLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR  
HPQDPCSSDAGRKRGPCTPAPTGSAFLSFIPRHFRPKAGSTTVKIVLKEKKKACVHGGKTYS  
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTEYPCRHPEKVAGKCKKICCPEDKADPGHSE  
ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH  
SQNLPLDSDQESQEARNPERGTALPTARWPPRSLERLPSDPGAEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

## **FIGURE 83**

GACAGCTGTGTCGATGGAGTAGACTCTCAGAACAGCGCAGTTGCCCTCGCTCACGCAGAGCCTCTCC  
GTGGCTTCCGCACCTGAGCATTAGGCAGTTCTCTCTCTCTAATCCATCCGTACCTCTCTGTCA  
TCCGTTCCATGCCGTGAGGTCCATTACAGAACACATCCTGGCTCTCATGCTCAGTTGGTTCTGAGTC  
TCCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTGGGCCAGACAAGCCTGTCAGGCCCTGGTGGGGAG  
GACGCAGCATTCTCTGTGTTCCCTAAGACCAATGCAGAGGCCATGAAAGTGCGGTTCTCAGGG  
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTATGCAGATGCCACAGTATC  
AAGGCAGGACAAAATGGTGAAGGATTCTATTGCGGAGGGCGCATCTCTGAGGCTGGAAAACATTACT  
GTGTTGGATGCTGCCCTCATGGTGCAGGATTAGTTCCCAGTCTTAACCAGAAGGCCATCTGGGAGCT  
ACAGGTGTCAGCACTGGGCTCAGTTCTCATTTCCATCACGGGATATGTTGATAGAGACATCCAGCTAC  
TCTGTCAGTCCTCGGGCTGGTCCCCGGCCACAGCGAAGTGGAAAGGTCACAAGGACAGGATTTGTC  
ACAGACTCCAGGACAAAACAGAGACATGCATGGCCTGTTGATGTGGAGATCTCTGACCGTCCAAGAGAA  
CGCCGGGAGCATATCCTGTTCCATGCCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG  
GAGATACCTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGAATACTCTGCTGTGGCTA  
TTTTTGGCATTGTTGGACTGAAGATTTCTCTCCAAATTCCAGTGGAAAATCCAGGGGAACTGGACTG  
GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGAAACACGCAGTGGAGGTGACTCTGGATCCAG  
AGACGGCTCACCGAAGCTCGCTTCTGATCTGAAACTGTAACCCATAGAAAGCTCCCAGGAGGTG  
CCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGCTCTCAGAGTTCCAAGCAGGGAAACATTA  
CTGGGAGGTGGACGGAGCACAAATAAAAGTGGCGCTGGAGTGTGCGGGATGATGTGGACAGGAGGA  
AGGAGTACGTGACTTTGTCTCCGATCATGGTACTGGTCTCAGACTGAATGGAGAACATTGTATTTC  
ACATTAATCCCCGTTTATCAGCGTCTCCCCAGGACCCACCTACAAAAAATAGGGTCTCTGGACTA  
TGAGTGTGGACCACCTCCTCTTCAACATAATGACCAGTCCCTTATTATACCCCTGACATGTCGGTTG  
AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAATGGAACATCCCATAGTCATG  
CCAGTCACCCAGGAATCAGAGAACAGGGCTCTGGCAAAGGGCCTCTGCAATCCCAGAGAACAG  
TGAGTCCTCCTCACAGGCAACCACGCCCTCCCTCCCCAGGGTGAATGTAAGGATGAATCAACATCCCACAT  
TCTTCTTAGGGATATTAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCCGGCAAGGTGGCTTCCA  
GATGAAGGGGACTGGCTGTCCACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGAGGGAAAGAAG  
CTGACATTACATTAGTTGCTCTCACTCCATCTGGCTAAGTGAATCTTGAATACCACCTCTCAGGTGAAG  
AACCGTCAGGAATTCCCATCTCACAGGCTGTGGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAG  
ATCTTATTGATGACAGAGTGTATCCTAATGGTTGTTCAATTACACTTTCAGTAAAAAA

## **FIGURE 84**

MALMLSLVLSLLKLGSQWQVFQPDKPVQALVGEDAASFCLSPKTNAEAMEVRFFRGQFSSVH  
LYRDGKDQPFMQMPPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYYQKAIWELO  
VSALGSVPPLISITGYVDRDIQLLCQSSGWFPRPTAKWKGPOQGQDLSTDRTNRDMHGLFDVEISL  
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK  
FQWKIQAELDWRRKHGQAEELDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAPEVPHSEKRF  
TRKSVVASQSFFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLSPDHGYWVRLNGEHLYFT  
LNPRFISVFPPRTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT  
PIVICPVTQESEKEASWQRASAIPETSNSESSSQATTPFLPRGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255

## **FIGURE 85**

AACAGACGTTCCCCCGCGGGCCCTGGCACCTCTAACCCCCAGACATGCTGCTGCTGCTGCTGCCCT  
GCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTTCCGTGA  
CGGTGCAGGAAGGCCGTGTGTCATGTGCCCTGCTCCTCTCCATCCCGCATGGCTGGATT  
TACCCCTGGCCCAGTAGTCATGGCTACTGGTCCGGAAAGGGCCAATACAGACCAGGATGCTCC  
AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGCTCGGGACCGATTCCACCTCCTTG  
GGGACCCACATACCAAGAATTGCACCCGTGAGCATCAGAGATGCCAGAAGAAGTGTGCGGGAGA  
TACTTCCTTCGTATGGAGAAAGGAAGTATAAAATGAAATTATAAACATACCGGCTCTGTGAA  
TGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCCGAGGACCCCTGGAGTCGGCTGCC  
AGAACATGACCTGCTCTGTGCCCTGGCCTGTGAGCAGGGACACCCCTATGATCTCCTGGATA  
GGGACCTCCGTGTCCCCCCTGGACCCCTCACCACCCGCTCCGGCTCACCCCATCCCACA  
GCCCGAGGACCATGGCACCAAGCCTCACCTGTCAGGTGACCTCCCTGGGCCAGCGTGACCA  
ACAAGACCGTCCATCTCAACGTGTCCTACCCGCTCAGAACATTGACCATGACTGTCTCCAAGGA  
GACGGCACAGTATCCACAGTCTTGGAAATGGCTCATCTGTCACTCCAGAGGGCAGTC  
GCGCCTGGTCTGTGCAAGTTGATGCAAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGA  
GAGGCCTGACCTGTGCCCTCACAGCCCTCAAACCCGGGGTGCTGGAGCTGCCTGGGTGCAC  
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCCCTCGGCTCTCAGCAGGTCTACCT  
GAACGTCTCCCTGCAGAGCAAAGCCACATCAGGAGTGA  
CTCAGGGGGTGGTCGGGGAGCTGGAG  
CCACAGCCCTGGCTTCCTGTCCTCTGCCATCTTCGTTGAGGTCCTGCAGGAAGAAA  
TCGGCAAGGCCAGCAGCGGGCGTGGAGATA  
CAGGGCATAGAGGATGCAAACGCTGTCAGGGGTT  
AGCCTCTCAGGGGCCCTGACTGAACCTGGCAGAACAGACTCCCCAGACCAGCCTCCCCAG  
CTTCTGCCGCTCCTCAGTGGGGAGGAGGCTCCAGTATGCATCCCTCAGCTCCAGATGGT  
AAGCCTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG  
ATGGAGAAACTGCAGAGACTCACCCGTGATTGAGGGATCACAGCCCTCCAGGCAAGGGAGAAGTCA  
GAGGCTGATTCTGTAGAATTAAACAGCCCTAACGTGAGCTATGATAACACTATGAATTATG  
TGCAGAGTGAAAGCACACAGGCTTAGAGTCAAAGTATCTAAACCTGAATCCACACTGTGCC  
TCCCTTTATTTTTAACTAAAAGACAGACAAATTCTCA

## **FIGURE 86**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTQEGLCVHPCFSYPSHGWIYPGPVVHGYWFREG  
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNTLSIRDARRSDAGRYFFRMEKGSIKWNY  
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSVPWACEQGTPPMISWIGTSVSPLDPSTTRS  
SVLTLIPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLTMVFQGDGTVSTVLGNSSL  
SLPEGQSLRLVCADVDAVDNSPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP  
LGSQQVYLNVSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDTGIE  
DANAVRGSASQGPLTEPWAEDSPPDQPPPASARSSVGEGELOQYASLSFQMVKPWDSRGQEATDTE  
YSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

## **FIGURE 87**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTGTAC  
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAAATGAACCAACTCAGCTTCCTGCTGTTTC  
TCATAGCGACCACCAAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT  
TCTTCGTCATCCATCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTGA  
TGGCCTGTATTTCTCCGCACTGAGAATGGTGTATCTACCAAGACCTCTGTGACATGACCTCTG  
GGGGTGGCGGCTGGACCCCTGGTGGCCAGCGTGATGAGAATGACATGCGTGGGAAGTGCACGGT  
GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGACGGCAACTGGC  
CAACTACAACACCTTGGATCTGCAGAGGCCACGAGCGATGACTACAAGAACCCCTGGCTACT  
ACGACATCCAGGCCAAGGACCTGGCATCTGGCACGTGCCAATAAGTCCCCATGCAGCACTGG  
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTCCTCCAGACACTGGGACATAATCT  
GTTTGGCATCTACCAGAAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC  
CGGTGATCCCTGTGGTCTATGATTTGGCGACGCCAGAAAACAGCATCTTATTACTCACCCCTAT  
GGCCAGCGGAATTCACTGCGGGATTGTTCAAGGGTATTAATAACGAGAGAGCAGCCAA  
CGCCTTGTGCTGGAATGAGGGTACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG  
GATACTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTCTGGTTTGATTGGAGTGGATATCG  
GGAACTCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG  
TTGAGAGTTTGTGGAGGGACCCAGACCTCTCCACCAGATGAGATCCCAAGGATGGAGAA  
CAACTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGA  
AAAAAA

## **FIGURE 88**

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI  
YQTFCDMTSGGGGTLVASVHENDMRGKCTVGDRSSQQGSKADYPEGDGNWANYNTFGSAEAAT  
SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYG  
EGKCWTNDGPVIPVVYDFGDAQKTASYYSPYGQREFTAGFVQFRVFNNERAANALCAGMRVTGCN  
TEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSSREITEAAVLLFYR

**Important features:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation site.**

amino acids 163-167

**Glycosaminoglycan attachment sites.**

amino acids 74-78, 289-293

**N-myristoylation sites.**

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

## FIGURE 89

CTAGATTGTCGGCTTGC~~GGGGAGACTTCAGGAGTCGCTGTCTGAAC~~TCCAGCCTCAGAGAC  
CGCCGCCCTGTCCCCGAGGGCATGGGCCGGTCTCAGGCTTGCCCTCGCTTCTGACG  
CTCCTGGCGCATCTGGTGGT~~CGTCATCACCTTATTCTGGTCCC~~GGACAGCAACATA~~CAGGC~~CTG  
CCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATT~~CAGCTGGTGGCCG~~CTC  
CTGTCACCCTGGGCTCTTGAGTGGAGCTGGCCGGTTCTCAGGAGTCTCCATGTTAAC  
AGCACCCAGAGCCTCATCTCATTGGGCTCACTGTAGTGCATCCGTGGCCCTGT~~CC~~TCTTCAT  
ATT~~CGAGCG~~TTGGGAGTGC~~ACTACGTATTGTACATT~~TTGTCT~~CGCAGTGC~~CCCTTCCAGCTG  
TCACTGAAATGGCTTATT~~CGTCACCGTCTTGGG~~CTGAAAAAGAAACCC~~CTGATT~~ACCTTCA  
TGACGGAAC~~CTAAGGACGAAGC~~CTACAGGGCAAGGGCGCTCGTATT~~CCTGGA~~AGAAGGAAG  
GCATAGGCTTCGGTTTCCCCTCGAAA~~CTGCTG~~CTGGAGGATATGTGTTGGAATAATTACG  
TCTTGAGTCTGGATTATCCGATTGTATTAGT~~GCTTGT~~AATAAAATGTTTGTAGTAACA  
TTAAGACTTATATA~~CAGTTTAGGGACAATT~~AAAAAAAAAAAAAA

## **FIGURE 90**

MGRVSGLVPSRFLTLAHLVVVITLFWSRDSNIQACLPLTPEEYDKQDIQLVAALSVTLGLFA  
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVTEMALFV  
TVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

## **FIGURE 91**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGGAGAGCGGGAGGAAGATGCAACTGAC  
TCGCTGCTGTTCTGTGTCAGGGTAGCCTCTATCTGGTATCTGTGCCAGGATGATG  
GTCCTCCCGGCTCAGAGGACCTGAGCGTATGACCACGAGGGCAGCCCCGGGGTGCCT  
CGGAAGCGGGGCCACATCTACCTAACGCCCAGGCCATTCCACTCTCCTAGGGCTGCT  
GGCCCCGCTGGGAGGCTTGGGCATTCTGGCAGCCCCAACGCCGAACCACAGCCCC  
CACCCCTCAGCCAAGGTGAAGAAAATCTTGCTGGGCACTTCACTCCAACTCAAGACGGTG  
GCCCTGAACCTGCTCGTCACAGGGAAAGATTGTGGACCATGGCAATGGACCTTCAGCGTCCACTT  
CCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTCCCCCAGTAAAGCTGTAG  
AGTTCCACCAGGAACAGCAGATCTCATCGAAGCCAAGGCCTCCAAATCTCAACTGCCGGATG  
GAGTGGGAGAAGGTAGAACGGGCCGGACCTCGCTTGACCCACGCCAGCCAAGATCTG  
CTCCCCGAGACCACGCTCAGAGCTCAGGCCACCTGGAGCTGCTCCAGCCCTCAAAGTCGTGTG  
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCAGATTACAACATAC  
CATAGTGATAACCCCTACTACCCATCTGGTGACCCGGGCAGGCCACAGAGGCCAGGGC  
TGGAAAGGACAGGCCATGCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAAGGGTTGGCCTC  
AGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGCCAGGGCAAGTCTCAAGTGGCAG  
AGAAAGGGTCCAAGTGCTGGTCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGG  
AGGAGGAGTGGCTCTCTGTGCAGCCTCACAGGGCTTGCCACGGAGCCACAGAGAGATGCTGG  
TCCCCGAGGCCGTGGCAGGCCATCAGTGTCAGGAGCTTGGCCAGATCAAGTCATGGAGGAAGCTAAC  
CCTTGTTCTGCATCCTGAGGAAAGATAGCAACAGGGAGGGAGATTTCATCAGTGTCAG  
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCTTAGGAGCCAGTCAGCAGGGTGGGTGG  
GCCAGAGGAGCTCCAGCCCTGCCTAGTGGCGCCCTGAGCCCTTGTGTCGTGAGCATGG  
CATGAGGCTGAAGTGGCAACCCCTGGGTCTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC  
CAGGCCACCCCTTCCAAAATCCCTCTTGCCAGTACTCCCCCTGTACCAACCCATTGCTGATG  
GCACACCCATCCTTAAGCTAACGACAGGAGGATTGTGGCTCCACACTAACGGCACAGCCCCATC  
CGCGTGTGTGTGTCCTCTCCACCCCTGCTGGCTCTGGAGCATCCATGTCCCG  
GAGAGGGGTCCCTAACAGTCAGCCTCACCTGTCAGACCGGGGTTCTCCGGATCTGGATGGCG  
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGCCAGAGCATGTGCTGGATCTGTT  
TGTGTGTCTGTCTGTGGTGGGGAGGGAGGGAAAGTCTTGAAACCGCTGATTGCTGACTTT  
TGTGTGAAGAATCGTGTCTTGAGCAGGAAATAAGCTTGGCCGGGGCA

## FIGURE 92

MQLTRCCFVFLVQGSILYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL  
LGLLAPPGEAWGILGQPPNRPNHSPPPSAVKKI~~FGWGD~~FYSNIKTVANLLVTGKIVDHGN  
SVHFQHNATGQGNISISLVPPSKAVEFHQQQIFIEAKASKIFNCRMEWEKVERGRRTSLCTHDP  
AKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC~~D~~NYHSDTPYYPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

### **FIGURE 93**

CGGTGGCCATGACTGCGGCCGTGTTCTCGGCTGCGCCTCATTCGCTTCGGGCCTGCGCTGCC  
CTTATGTCTCACCATGCCATCGAGCCGTTGCGTATCATCTTCCTCATGCCGGAGCTTCTT  
CTGGTTGGTGTCTACTGATTCTGTCCTGTTGGTCATGGCAAGAGTCATTATTGACAACA  
AAGATGGACCAACACAGAAATATCTGCTGATCTTGAGCCTTGTCTGTCTATATCCAAGAA  
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAAGCCAGTGAAGGTTGAAGAGTATAAACCC  
AGGTGAGACAGCACCCCTCATGCGACTGCTGGCCTATGTTCTGGCTGGGCTTGGATCATGA  
GTGGAGTATTTCCCTTGTAATACCTATCTGACTCCTTGGGCAAGGCACAGTGGCATTGAT  
GGAGATTCTCCTCAATTCTCCTTATTCACTGCTGGTCATTATCTGCTGATGT  
ATTCTGGGCATTGATTTTGATGGCTGTGAGAAGAAAAAGTGGGCATCCTCCTATCGTTC  
TCCTGACCCACCTGCTGGTGTCAAGCCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG  
TCAGCATTATAATCCTGGTGTCACTGGCACCTGGCATTCTAGCTGCGGGAGGCAGCTGCCG  
AAGCCTGAAACTCTGCCTGCTTGCAAGACAAGAACTTCTTACAACCAGCGCTCCAGAT  
AACCTCAGGGAACCAAGCACTTCCAAACCGCAGACTACATCTTAGAGGAAGCACAACGTGCCT  
TTTCTGAAAATCCCTTTCTGGTGAATTGAGAAAGAAATAAACTATGCAGATA

## FIGURE 94

MTAAVFFGCAFIAGPALALYVFTIAIEPLRIIFLIAGAFFWLVSIILISSLVWFMARVIIDNKDG  
PTQKYLLIFGAFVSYYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV  
FSFVNNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKW GILLIVLLT  
HLLVSAQTFISSYYGINLASAFIILVIMGTWAFLAAGGSCRSLKLCLLCQDKNFLLYNQRSR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

## FIGURE 95

AATTTTCACCAGAGTAAACTTGAGAACCAACTGGACCTTGAGTATTGTACATTTGCCTCGTG  
GACCCAAAGGTAGCAATCTGAACATGAGGAGTACGATTCTACTGTTTGTCTTAGGATCAAC  
TCGGTCATTACCACAGCTCAAACCTGCTTGGGACTCCCTCCACAAAACTGGCTCCGGATCAGG  
GAACACTACCAAAACCAACAGCAGTCAAATCAGGTCTTCCTCTTAAGTCTGATACCATTAACA  
CAGATGCTCACACTGGGCCAGATCTGCATCTGTTAACCTGCTGCAGGAATGACACCTGGTAC  
CCAGACCCACCCATTGACCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC  
CAATTTTGTCAACAACTTGAGCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC  
TTCACGAGCCTCATCCATTCTGTTCCGGAGGCATCCTGCCACCAGTCAGGCAGGGC  
TAATCCAGATGTCCAGGATGGAAGCCTCCAGCAGGAGGAGCAGGTGAAATCCTGCCACCCAGG  
GAACCCCAGCAGGCCGCCTCCAACTCCCAGTGGCACAGATGACGACTTGAGCACCACCCCT  
GCAGGCATCCAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA  
GTAAGCTTTCAAATTTCCAACTAAGCTGCCCGAATTGGTATACATGTGAATCTTATC  
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATT  
TACCTGAAAATATTCTGAAATTCAGAAAATATGTTCTATGTAGAGAATCCAACTTTAAAAAA  
CAATAATTCAATGGATAAAATCTGTCTTGAAATATAACATTATGCTGCCGGATGATATGCATAT  
TAAAAACATATTGAAAAACTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 96**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSSLIPLTQM  
LTLPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRPLPTPSG  
TDDDFAVTTPAGIQRSTHAIIEATTESANGIQ

**Signal peptide:**

amino acids 1-16

## **FIGURE 97**

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT  
CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGCGCTGGAGGGCTGTGACCATG  
GTCCTGCCTGGCTGGCTGCTTGTGTCCTCCGTCcccAGGCTCTCCCAAGGCCAGCCTGC  
AGAGCTGTCTGTGAAAGTTCCAGAAAATATGGTGGAAATTCCCTTATACTGACCAAGTGTG  
CGCTGCCCGTGAGGGGCTGAAGGCCAGATCGTGTGTCAGGGACTCAGGCAAGGCAACTGAG  
GGCCCATTTGCTATGGATCCAGATTCTGGCTTCTGCTGGTGAACAGGGCCCTGGACCGAGAGGA  
GCAGGCAGAGTACCGAGCTACAGGTACCCCTGGAGATGCAGGATGGACATGTCTTGTGGGTCAC  
AGCCTGTGCTTGTGACGTGAAGGATGAGAATGACCAGGTGCCCCATTCTCTCAAGCCATCTAC  
AGAGCTGGCTGAGCCGGGTACCAAGGCCCTGGCATCCCCCTCTCCTTGAGGCTTCAGACCG  
GGATGAGCCAGGCACAGCCAATCGGATCTCGATTCCACATCTGAGCCAGGCTCCAGGCCAGC  
CTTCCCCAGACATGTTCCAGCTGGAGCCTGGCTGGGCTCTGGCCCTCAGCCCCAAGGGGAGC  
ACCAGCCTTGACCCAGGCCACTGGAGAGGACCTACCGAGCTGGTACAGGTCAAGGACATGGGTGA  
CCAGGCCCTCAGGCCACCAGGCCACTGGCACCGTGGAAAGTCTCCATCATAGAGGACACCTGGGTG  
CCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCTTACCCGACCCACATGGCCAGGTA  
CACTGGAGTGGGGGTGATGTGCACTATCACCTGGAGAGCCATCCCCGGGACCTTGAAGTGA  
TGCAGAGGGAAACCTCTACGTGACCGAGAGGACCTGGAGAGGACTATGCGCCCCCTCTGGAGCTGACGTGCTG  
AGGTGGGGCTCAGAAATTCCATGGCAGGAGACTATGCGCCCCCTCTGGAGCTGACGTGCTG  
ATGGATGAGAATGACAACGTGCTTACCTGGCTTACGGTGTGACGCTGGGGCTCCACTCCGAGCAGGCCAGAACAT  
CCTGCTCTGGTGTGGCATGGACCTGGCAGGGCAGAGGGTGGCTTCAGCAGCACGTGTA  
TCGAAGTCGAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCAGATTGGCCT  
ATAAGCTCCCTGAGGATGTGGAGCCGGACTCTGGTGGCCATGCTAACAGCATTGATGCTGA  
CCTCGAGCCCGCCTCCGCTCATGGATTGCAATTGAGAGGGGAGACACAGAAGGGACTTTG  
GCCTGGATTGGGAGGCAGACTCTGGGATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG  
GCAGCTCAAGTCATGAGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCAGGCC  
AGGCCCTGGAGCCACGCCACGGTACTGTCCCCATCAGTGCCTCAGGGCTCTTCTGCTGACCATC  
ACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCTCAGGGCTCTTCTGCTGACCATC  
CAGCCCTCCGACCCCATCAGCCGAACCTCAGTTCTCCCTAGTCATGACTCAGAGGGCTGGCT  
CTGCATTGAGAAATTCTCCGGGGAGGTGCACACCGCCAGTCCCTGCAGGGGCCAGCTGGG  
ACACCTACACGGTCTTGTGGAGGGCCAGGATAACGCCCTGACTCTGCCCCCTGTGCCCTCCAA  
TACCTCTGCACACCCGCCAAGACCATGGCTGATGCTGAGTGGACCCAGCAAGGACCCGATCT  
GGCCAGTGGGACGGTCCCTACAGCTTACCCCTGGTCCCAACCCACGGTGCACGGGATTGGC  
GCCTCCAGACTCTCAATGGTCTCCATGCCCTACCTCACCTGGCCCTGCAATTGGTGGAGGCCAGT  
GAACACATAATCCCGTGGTGGTCAAGCCACAATGCCCAAGATGTGGCAGCTCCCTGGTGGAGTGT  
CGTGTGCGCTGCAACGTGGAGGGCAGTGCATGCGCAAGGTGGGGCGCATGAAGGGCATGCCA  
CGAAGCTGTGGCAGTGGCATCCTGTAGGCACCCCTGGTAGCAATAGGAATCTTCTCATCCTC  
ATTTTACCCACTGGACCATGTCAGGAAGAAGGACCCGATCAACCCAGCAGACAGGGTGC  
GAAGGGACTGTCTGAATGGCCACGGCAGCTAGCTGGAGGCTTGGCCTCTGGCTCCATCTGAG  
TCCCTGGGAGAGAGGCCAGCACCAAGATCCAGCAGGGACAGGAGCTAGAAGGCCCTCCA  
TCTGCCCTGGGGTGAGGGACCCATCACCACCAAGGGCATGTCAGAGCCTGGACACCAACTT  
TATGGACTGCCCATGGAGGTGCTCCAAATGTCAGGGTGTGCCCCATAATAAGCCCCAGAGAA  
CTGGGCTGGGCCATGGAAAAAAGAAAAAAAAAAGAAAAAAAAAAG

## **FIGURE 98**

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSKAT  
EGPFAMDPDSGFLLVTRALDREEQAELYQLQVTLEMQDGHVLWGPQPVLHVKDENDQVPHFSQAI  
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPDMFQLEPRLGALALSPKG  
STS LDHALERTYQLLVQVKDMGDQASGHQATATVEVSIIESTWVSLEPIHLAENLKVLYPHHMAQ  
VHWSSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQEYLLQVRAQNSHGEDYAAPPLELHVL  
VMDENDNVPICPPRDPTVSIPELSPPGTEVTRLSAEDADAPGSPNSHVYQLLSPEPEDGVGRA  
FQVDPTSGSVTLGVPLPLRAGQNILLVLAMDLAGAEGGSSTCEVEAVTDINDHAPEFITSQIG  
PISLPEDVEPGTLVAMLTAIDADLEPAFRIMDFAIERGDTEGTFGILDWEPSGHVRLRLCKNLSY  
EAAPSHEVVVVVQSVAKLGVPGPGPATATVTLVERVMPPPQLDQESYEASVPISAPAGSFLLT  
IQPSDPISRTLRFSLVNDSEGWLICIEKFSCGEVHTAQSLQGAQPGDTYTVLVEAQDTALTLPVPS  
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPETVQRDWRLQTLNGSHAYLTIALHWEP  
REHITPVVVSHNAQMWWQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTILVAIGIFLI  
LIFTHTWMSRKKDPDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

## **FIGURE 99**

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACGCC  
AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCACAGCTCTGGAAAGCACAGCCTTTA  
TCTCTTCAACCTTCAGTCCCCCTTCTCAAGAATCCTCTGTTCTTGCCTCTAAAGTCTTGGTAC  
ATCTAGGACCCAGGCATCTTGCTTCCAGCACAAGAGACAGATGAAGATGCAGAAAGGAATG  
TTCTCCTTATGTTGGTCTACTATTGCATTAGAAGCTGCAACAAATTCCAATGAGACTAGCACC  
TCTGCCAACACTGGATCCAGTGTGATCTCAGTGGAGCAGCACAGCCACCAACTCTGGGTCCAG  
TGTGACCTCCAGTGGGTCAAGCACAGCCACCATCTCAGGGTCCAGCGTGAACCTCCAATGGGTCA  
GCATAGTCACCAACTCTGAGTCCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG  
TTCAGCACAGCGTCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACCTCCAGTGG  
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCCTCAGTGGGCCAGCACAGTCACCAACT  
CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCAGTGCACCAACTCTGAGTCCAGCACAGTGTCC  
AGTAGGGCCAGCAGTGCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGCCAGCACAGCCAC  
CAACTCTGACTCCAGCACAACCTCCAGTGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCAGT  
GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAG  
AACGACCTCAATGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGCCA  
GCACAGCCACCAACTCTGACTCCAGCACAGCCACCAACTCTGAGTCCAGTAGGGCCAGCAGTGC  
TCCAGCACGACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG  
GGCTAGCACAGCCACCAACTCTGACTCCAGCACAAACCTCCAGTGGGCCAGCACAGCCACCAACT  
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCCTC  
AGTGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGCCAACACAGCCAC  
CAACTCTGAGTCCAGCACAGTGTCCAGTGGGCCAGCAGTGCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGTCAAGCACAGCCACCAACTCTGAGTCCAGCACAAACCTCCAGTGGGCCAGCACA  
GCCACCAACTCTGACTCCAGCACAAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCTAG  
CACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAAACCTCCAGTGGGCCA  
ACACAGCCACCAACTCTGGGTCAGTGTGACCTCTGCAGGCTCTGAACAGCAGCTCTGACTGGA  
ATGCACACAACCTCCATAGTCATCTACTGCAGTGAGTGAGGCAAAGCCTGGTGGTCCCTGGT  
GCCGTGGAAATCTTCTCATACCCCTGGCTCGGTTGTGGCGCGTGGGCTCTTGCTGGC  
TCTTCTCTGTGTGAGAAACAGCCTGCTCCCTGAGAAACACCTTTAACACAGCTGTCTACCACCC  
CATGGCCTCAACCATGGCCTGGTCCAGGCCCTGGAGGAAATCATGGAGCCCCACAGGCCAG  
GTGGAGCTTAACCTGGTCTGGAGGAGACCAAGTATCGATAGCCATGGAGATGAGCGGGAGGA  
ACAGCGGGCCCTGAGCAGCCCCGGAGCAAGTGCAGCATTCTCAGGAAGGAAGAGACCTGGCA  
CCCAAGACCTGGTTCTTCTTCAATTCTACCCAGGAGACCCCTCCAGCTTGTGAGATCTGAA  
AATCTTGAAGAAGGTATTCTCACCTTCTGCCTTACAGACACTGGAAAGAGAAACTATAT  
TGCTCATTTAGCTAAGAAATAACATCTCATCTAACACACAGCACAAAGAGAAGCTGTGCTTG  
CCCCGGGTGGGTATCTAGCTGAGATGAACCTCAGTTATAGGAGAAAACCTCCATGCTGGACTC  
CATCTGGCATTCAAAATCTCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 100**

MKM**Q**GNVLLM**F**LLLH**E**ATNSNETSTSANTGSSVISSGASTATNGSSVTSGVSTATISGS  
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS  
GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNDSSTTSSGASTA  
TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSES  
STTSSGASTATNDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNDSSTTSS  
GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA  
TNSESSTTSSGVSTATNSESSTTSSGASTATNDSSTTSSSEASTATNSESSTVSSGISTVTNSES  
STTSSGANTATNGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA  
AVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGENHGAPHRPRWSPNWFWRPPVSSI  
AMEMSGRNNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

## **FIGURE 101**

GGCCGGACGCCTCCCGTTACGGGATGAATTAAACGGCGGTCCGCACGGAGGTGTGACCCCTA  
CGGAGCCCCAGCTTGCACGCACCCCACACTCGCGTCGCGCGCGTGCCTGCTGTACAGGTG  
GGAGGCTGAACTATCAGGCTGAAAAACAGAGTGGGTACTCTCTGGGAAGCTGGCAACAAAT  
GGATGATGTGATATATGCATTCCAGGGGAAGGGAAATTGTGGTGCTCTGAACCCATGGTCAATT  
AACGAGGCAGTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAGCTTGGAAATCAT  
GGTGTCATGGAAAGGGATTTACTTACTGACTCTGTTGGGAAGCTTTGGAAAGCATT  
TCATGCTGAGTCCCTTTACCTTGATGTTGTAACCCATCTGGTATCGCTGGATCAACAAAC  
CGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCATGTTGGTGTAAAAGT  
GATTATAACTGGGGATGCATTGTTCTGGAGAAAGAAGTGTCAATTATCATGAACCATCGGACAA  
GAATGGACTGGATGTTCTGTGGAATTGCGATAGCTACCTCAGATTGGAGAAAATT  
TGCCTCAAAGCGAGTCTCAAAGGTGTTCTGGATTGGTGGCCATGCAGGCTGCTGCCTATAT  
CTTCATTCA TAGGAAATGGAAGGATGACAAGAGCCATTGAGACATGATTGATTACTTTGTG  
ATATTCA CGAACCACTCAACTCCTCATATTCCAGAAGGGACTGATCTCACAGAAAACAGCAAG  
TCTCGAAGTAATGCAATTGCTGAAAAAAATGGACTTCAGAAATATGAATATGTTTACATCCAAG  
AACTACAGGCTTACTTTGTGGTAGACCGCTAAGAGAAGGTAAGAACCTTGTGCTGTCCATG  
ATATCACTGTGGCGTATCCTCACAAACATTCTCAATCAGAGAACGACCTCCTCCAAGGAGACTTT  
CCCAGGGAAATCCACTTCA CGGTCCACCGGTATCCAATAGACACCCCTCCCACATCCAAGGAGGA  
CCTTCAACTCTGGTGCCACAAACGGTGGAAAGAGAAAGAAGAGAGGCTGCGTTCTTCTATCAAG  
GGGAGAAGAATTTTATTACCGGACAGAGTGTCA TCCACCTTGCAGTCTGAAGTCTGAACCTGGTC  
CTTGTGGTCAAATTGCTCTATACTGTATTGGACCTGTTAGCCCTGCAATGTGCCTACTCAT  
ATATTGTACAGTCTGTTAAGTGGTATTATAATCACCATTGTAATCTTGCTGCAAGAGA  
GAATATTGGTGGACTGGAGATCATAGAACCTGCACTGGACTTTACACAAACAGCCACAT  
TTAAATTCAAAGAAAAATGAGTAAGATTATAAGGTTGCCATGTGAAAACCTAGAGCATATTG  
GAAATGTTCTAAACCTTCTAAGCTCAGATGCATTGCACTGGACTATGTCGAATATTCTTACT  
GCCATCATTATTGTTAAAGATATTGCACTTAATTGTGGAAAATATTGCTACAATT  
TTAATCTCTGAATGTAATTGATACTGTGTACATAGCAGGGAGTGTGATCGGGGTGAAATAACTT  
GGGCCAGAATATTAAACAATCATCAGGCTTTAAA

## **FIGURE 102**

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSFGIMVSWKGIYFILTLFWGSFFGSIFMLSP  
FLPLIMFVNPSWYRWINNRLVATWLTPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM  
FLWNCLMRYSYLRLKEICLKASLGVPFGFWAMQAAAYIFIHRKWKKSHFEDMIDYFCDIHEP  
LQLLIFPEGTDLTENSRSNAFAEKNGLQKYEYVLHPRTTGFTFVVDRREGKNLDLVHDITVA  
YPHNIPQSEKHLLQGDFPREIHFHVRYPIDLPTSKEDLQLWCHKRWEEKERLRSFYQGEKNF  
YFTGQSIPPCKSELRLVVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG  
LEIIIELACYRLLHKOPHLNSKKNE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

## **FIGURE 103**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCCACGGCTCTGCGCCTGAGACAGCTGGCTGACC  
TCCAAATCATCCATCCACCCCTGCTGTCACTGTTTCATAGTGTGAGATCAACCCACAGGAATA  
**TCCATGGCTTTGTGCTCATTGGTTCTCAGTTCTACGAGCTGGTGTCAAGGACAGTGGCAAGT**  
CACTGGACCGGGCAAGTTGTCAAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCTGCTCCCTCT  
TTCCTGAGACCAGTGCAGAGGCTATGGAAGTGCAGGTTCTCAGGAATCAGTTCCATGCTGTGGTC  
CACCTCTACAGAGATGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAACCTGA  
GTTTGTAAGGACTCCATTGCAGGGGGCGTGTCTCTAAGGCTAAAAACATCACTCCCTCGG  
ACATGGCCTGTATGGGTGCTGGTTCACTTCCCAGATTACGATGAGGAGGCCACCTGGGAGCTG  
CGGGTGGCAGCACTGGGCTCACTTCCATCGTGGGATATGTTGACGGAGGTATCCA  
GTTACTCTGCCTGCTCAGGCTGGTCCCCCAGGCCACAGCCAAGTGGAAAGGTCACAAGGAC  
AGGATTGTCTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGTTGGAGATCTCC  
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCATCCACCTGCTGAGCAGAGTCATGA  
GGTGGAAATCCAAGGTATTGATAGGAGAGACATTGTTCCACCTTGGCCTGGCTTCTA  
TTTACTCGGGTTACTCTGTTGGCTCTGTTGTTGATGGGATGATAATTGTTCTTC  
AAATCCAAGGGAAAATCCAGGGGAACTGGACTGGAGAAGAAAGCACGGACAGGCAGATTGAG  
AGACGCCCGGAAACACGCACTGGAGGTGACTCTGGATCCAGAGACGGCTACCCGAAGCTCGC  
TTCTGATCTGAAAATCTGTAACCCATAGAAAAGCTCCAGGGTTTCAAGCAGGGAGACATTACTGGGAGGTGGA  
TTTACAAGGAAGAGTGTGGTGGCTCTCAGGGTTTCAAGCAGGGAGACATTACTGGGAGGTGGA  
CGTGGGACAAAATGTAGGGTGGTATGTGGAGTGTGTCGGGATGACGTAGACAGGGGGAGAAC  
ATGTGACTTGTCTCCAAACATGGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTTC  
ACATTCAATCCCCATTATCAGCCTCCCCCAGCACCCCTCTACAGGAGTAGGGGTCTCCT  
GGACTATGAGGGTGGGACCATCTCCTTCTCAATACAAATGACCAGTCCATTATACCCCTGC  
TGACATGTCAGTTGAAGGCTTGTGAGACCCATATCCAGCATGCGATGTATGACGAGGAAAAG  
GGGACTCCCATATTCTATGTCAGTGTCTGGGATGAGACAGAGAACCCCTGCTAAAGGGC  
CCACACCCACAGACAGCACAGCCAAGGGAGGTGCTCCGACAGGTGGCCCAGCTTCTCT  
CCGGAGCCTGCGCACAGAGAGTCACGCCCTTACTCTCTTAGGGAGCTGAGGTTCTGCCC  
TGAGCCCTGCAGCAGGGCAGTCACAGCTCCAGATGAGGGGGATTGGCCTGACCCGTGGGAG  
TCAGAAGCCATGGCTGCCCTGAAGTGGGAGGAATAGACTCACATTAGGTTAGTTGTGAAAA  
CTCCATCCAGCTAACGCACTTGAACAAGTCACAACCTCCAGGCTCCTCATTGCTAGTCACGG  
ACAGTGATTCTGCTCACAGGTGAAGATTAAAGAGACAAACGAATGTGAATCATGCTTGCAGGTT  
TGAGGGCACAGTGTGCTAATGATGTGTTTATATTACATTCCCACCATAAACTCTGTT  
TGCTTATTCCACATTAATTACTTTCTCTATACCAAATACCCATGGAATAGTTATTGAACACC  
TGCTTGTGAGGCTCAAAGAATAAGAGGGAGGTAGGATTTTCACTGATTCTATAAGCCCAGCAT  
TACCTGATACAAAACCAGGCAAAGAAAACAGAAGAGGAAGGAAACTACAGGTCCATATCC  
CTCATTAACACAGACACAAAATTCTAAATAAAATTAAACAAATTAAACTAAACAATATTTA  
AAGATGATATATAACTACTCAGTGTGGTTGTCCCACAAATGCAGAGTTGGTTAATATTAAAT  
ATCAACCAAGTGTAAATTCAACATTAATAAGTAAAAAGAAAACCATAAAAAAAAAAAAAAA

## **FIGURE 104**

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH  
LYRDGEDWESKQMPQYRGRTEFKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR  
VAALGSLPLISIVGYVDGGIQLLCSSGWFPQPTAKWKGPGQGDLSSDSRANADGYSLYDVEISI  
IVQENAGSILCSIHLAEQSHEVESKVVLIGETFFQPSPWRLASILLGLLCGALCGVVMGMIIIVFFK  
SKGKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF  
TRKSVVVASQGFQAGRHYWEVDVGQNVGWWVGVCRDDVDRGKNNVTLSPPNNGYWVRLTTEHLYFT  
FNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLLRPYIQHAMYDEEKG  
TPIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

## **FIGURE 105**

CCTTCACAGGACTCTCATTGCTGGTGGCAATGATGTATCGCCAGATGTGGTGAGGGCTAGGAAAAGAG  
TTTGTGGAAACCCTGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTCCTGGCAGTGTGCATTGGA  
CTCACTGTTCATTATGTGAGATATAATCAAAGAAGACCTACAATTACTATAGCACATTGTCATTACAC  
TGACAAACATATGCTGAGTTGGCAGAGAGGCTTAACAATTACAGAAATGAGCCAGAGACTGGAAT  
CAATGGTAAAAATGCATTTATAAATCTCCATTAAGGAAAGAATTGTCAGTCTCAGGTTATCAAGTTC  
AGTCAACAGAACGATGGAGTGTGGCTCATATGCTGTTGATTGTAGATTCACTCTACTGAGGATCCTGA  
AACTGTAGATAAAATTGTCACGTGTTTACATGAAAGCTGCAAGATGCTGTAGGACCCCCTAAAGTAG  
ATCCTCACTCAGTTAAAATTAAAAAAATCAACAAGACAGAACACAGCTATCTAAACCATTGCTGCCGA  
ACACGAAGAAGTAAAACCTAGGTCAAGACTCAGGATCGTTGGGACAGAAGTAGAAGAGGGTGAATG  
GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGACACCTTAATTGCCACATGGC  
TTGTGAGTGCTGCTCACTGTTACAACATATAAGAACCTGCCAGATGGACTGCTTCCTTGGAGTAACA  
ATAAAACCTTCGAAATGAAACGGGTCTCCGAGAATAATTGTCATGAAAATACAAACACCCATCACA  
TGACTATGATATTCTCTGAGAGCTTCTAGCCCTACACAAATGCAGTACATAGAGTTGTC  
TCCCTGATGCATCCTATGAGTTCAACCAGGTATGTGATGTTGTGACAGGATTGGAGCACTGAAAAT  
GATGGTTTACAGTCAAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACAACTGCAATGAACC  
TCAAGCTTACAATGACGCCATAACTCCTAGAAATGTTATGTGCTGGCCTTACAGGAAAACAGATGCAT  
GCCAGGGGACTCTGGAGGACCCTGGTTAGTTCAAGATGCTAGAGATATCTGGTACCTGCTGGAAATAGTG  
AGCTGGGAGATGAATGTGCGAAACCCAACAAGCCTGGTTACTAGAGTTACGGCCTGCGGACTG  
GATTACTTCAAAACGGTATCTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTGTTTTG  
GGTGTGGAGGCCATTAGAGATACAGAAATTGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCA  
ATAAAACTGTTGCTGATGCATGATTTCTTCCAGCTGTTCCGACGTAAGCATCTGCTTCTGCCA  
GATCAACTCTGTCATCTGAGCAATAGTTGAAACTTATGTACATAGAGAAATAGATAATACAATATTAC  
ATTACAGCCTGTATTCAATTGTTCTCTAGAAGTTGTCAGAATTGACTTGTGACATAATTGTAAT  
GCATATATAACATTTGAAGCACTCCTTCTCAGTTCTCAGCTCCTCTCATTTCAGCAAATATCCATT  
TCAAGGTGCAGAACAGGAGTGAAAGAAAATATAAGAAGAAAAAAATCCCTACATTATTGGCACAGAA  
AAGTATTAGGTGTTCTTAGGAAATTAGAAATGATCATATTCAATTGAAAGGTCAAGCAAAGACA  
GCAGAATACCAATCACTCATTTAGGAAGTATGGAACTAAGTTAGGAAGTCCAGAAAGCAAGCCAG  
ATATATACCTTATTTCAATTCCAAACACTACTATGATAATGTGAAGAAGATTGTTGTGACCT  
ATAATAATTACAAACTTCATGCAATGTAATTGTCAGCAAATTAAAGCAAATATTATTAAACATTG  
TTACTGAGGATGTCAACATATAACAAATAAAATATAACACCA

## **FIGURE 106**

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTWHYVRYNQKKTYNYYSTLSFTTDKLY  
AEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSSQQKHGVLAHMLLICRFHSTED  
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG  
TEVEEGEWPWQASLQWDGSHRGCATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKGRL  
RRIIVHEKYKHPSHDYDISLAELSSPVPTNAVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS  
QNHLRQAQVTLIDATTNEPQAYNDAITPRMLCAGSLEGKTDACQGDGGPLVSSDARDIWYLAG  
IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)

## **FIGURE 107**

AGAGAAAGAAGCGTCTCCAGCTAACGCAATGCAGCCCTCCGGCTCTCGCGAAGAAGTTCCCTG  
CCCCGATGAGCCCCCGCGTGCCTCCCGACTATCCCAGGCAGGCGTGGGGACCGGGGCCAGC  
GCCGACGATCGCTGCCGTTTGCCTTGGGAGTAGGATGTTGAAGGATGGGGCTTCTCCCTT  
ACGGGGCTCACAATGGCCAGAGAAGATTGGTGAAGTGCTGCGCTGCTCACGCCCTCAA  
TCTGCTTTGGTAATGTCCATCAGTGTGTTGGCAGTTCTGCTGGATGAGGGACTACCTAA  
ATAATGTTCTCACTTAAC TGCAAGAACAGGGTAGAGGAAGCAGTCATTGACTTACTTCT  
GTGGTTCATCCGGTCATGATTGCTGTTGCTTCTTATCATTGTTGGGATGTTAGGATATTG  
TGGAACGGTGAAAAGAAATCTGTTGCTTCTGCTGGTACTTTGGAGTTGCTGTCATTCT  
GTGTTAGAACTGGCTGTGGCCTTGGACATATGAACAGGAACCTATGGTCCAGTACAATGGCA  
GATATGGTCACTTGAAAGCCAGGATGACAATTATGGATTACCTAGATATCGTGGCTTACTCA  
TGCTTGAATTTCAGAGAGTTAACGTTAGTGTGGAGTAGTATATTCACTGACTGGTGG  
AAATGACAGAGATGGACTGGCCCCCAGATTCTGCTGTTAGAGAATTCCAGGATGTTCCAAA  
CAGGCCACCAGGAAGATCTCAGTGACCTTATCAAGAGGGTTGTTGGAGAAAATGTTACCTT  
TTTGAGAGGAACCAAACAAC TGCAAGGTGCTGAGGTTCTGGAATCTCCATTGGGTCACACAA  
TCCTGGCATGTTCTCACCATTACTCTGCTCTGGCTCTGTTATGATAGAAGGGAGCCTGG  
ACAGACCAAATGATGTCCTGGAAGAATGACAACCTCAGCACCTGTCATGTCCTCAGTAGAACT  
GTTGAAACCAAGGCTGTCAAGAATCTTGAAACACATGCAAGCAGCTTAATACACACT  
TTGAGATGGAGGAGTTAAAGAAATGTCACAGAAGAAACCAACACTGTTTATTGGACT  
TGTGAATTGAGTACATACTATGTTTGAGAAATATGAGAAATTTGTTGCAATAAGTC  
TAACACCTAACATACTATTCTATGCTTAAAGGAGATGAAAGTTCTGTCATGTCATAAGTC  
ACCACCTGGACAATAATTGATGCCCTTAAAGGAGATGTCATACCCACTGTCAGGCC  
TGTGTATGACTTTACTGAACACAGTTATGTTTGAGGCGAGCATGGTTGATTAGCATTCCGCA  
TCCATGCAAACGAGTCACATATGGTGGACTGGAGCCATAGTAAAGGTTGATTACTTCTACCAA  
CTAGTATATAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAACTAATAACTTTTATT  
CTCAGCGATCTATTCTCTGATGCTAAATAAATTATATCAGAAAACCTTCATATTGGTACT  
ACCTAAATGTTGACTTCTGGCTGGTTACTAAATATTCTTACCACTTAAAGAGCAAGCTAACACAT  
TGTCTTAAGCTGATCAGGGATTGGTATATAAGTCTGTTAAATCTGATAATTCACTGAT  
TTCAGTTCTGATAATGTTAGAATAACCATTATGAAAAGGAAATTGTCCTGATAGCATT  
ATTGGTCTTCTGTTATGCTGATGCTAAATAAAGCTTACTATTCTGCTGGCTTATATTACACATATAAC  
TGTATTTAAATACCTAACACTAATTGAAAATTACCACTGTTGAGAATGACATAGGAATCATT  
AGAATGAGTCTGGCTTTAGGAAGTATTAATAAGAAAATTGACACATAACTTAGTTGATT  
AAGGACTTGTATGCTGTTTCTCCAAATGAAGACTTTTGACACTAAACACTTTAAAAAA  
GCTTATCTTGCCTCTCCAAACAGAAGCAATGTCAGTCATATAAATTCTACAGAAAA  
TAGTGTCTTTCTCCAGAAAATGCTGAGAATCTTAAACATGACAAATTAGAGATT  
CTTGTGTTATTTCACTGATAATATACTGTGGCAAATTACACAGATTATTAATTTTACAA  
GAGTATAGTATATTGAAATGGGAAAGTGCAATTACTGTGTTGTTGTTATTTGTTAT  
TTCTCAGAATATGAAAGAAAATTAAATGTGCAATAAAATATTCTAGAGAGTAA

## **FIGURE 108**

MAREDSVKCLRCLLYALNLLFWLMSISVLAWSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHP  
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT  
LKARMNTNYGLPRYRWLTHAWNFFQREFKCCGVVFWDWLEMTEMDWPPDSCCVREFPGCSKQAHQ  
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFGLISIGVTQILAMILTITLLWALYYDRREPGTDQM  
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

## **FIGURE 109**

CCAAGGCCAGAGCTGTGGACACCTTATCCCACCTCATCCTCATCCTCTTCCCTGATAAAGCCCCTACCAAGTGCT  
GATAAAAGTCCTTCTCGTAGAGGCCTAGAGGCCCTAAAAAAAAAGTCCTGAAAGAGAAGGGGACAAAGGAACA  
CCAGTATTAAAGAGGATTTCCAGTGTTCGGCAGTGGTCCAGAAGGATGCCTCCATTCCCTGCTTCTCACCTG  
CCTCTTCATCACAGGCACCTCCGTGTACCCGTGCCCTAGATCCTTGTCTGCTTACATCAGCCTGAATGAGC  
CCTGGAGGAACACTGACCACCAAGTGGATGAGTCAGTCAGGTCCTCTATGTGACAACCATGTGAATGGGAG  
TGGTACCACTTCACGGGCATGGCGGGAGATGCCATGCCACCTCTGCATACCAAGAAAACACTGTGGAACCC  
CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAGGCAGGCATTGTGCAACGCCAGGCTGTGCCAGCT  
TCAATGGGAACACTGCTGTCTGGAACACCACGGTGGAAAGTCAGGCTGCCCCTGGAGGCTACTATGTGTATCGT  
CTGACCAAGGCCAGCGCTGTCTCCACGCTACTGTGGTCAATTATGACATCTGCGACGAGGACTGCCATGG  
CAGCTGCTCAGATACCAGCGACTGCACATCGCCTCCAGGAACACTGTCTAGGCCCTGACAGGCACACATGCTTG  
ATGAAAATGAATGTGAGCAAACACCGTGGCTGCACTGAGATCTGTGTGAAACCTCAAAACTCTACCGCTGT  
GAGTGTGGGTTGGCGTGTGCTAAGAAGTGTGCAAGACTTGTGAAAGACGTTGAAGGATGCCACAATAACAA  
TGGTGGCTGCAGCCACTCTGCCTGGATCTGAGAAAGGCTACCAAGTGTGAAATGTCCCAGGGCTGGTGT  
CTGAGGATAACCAACACTTGCCTGGCAAGTCCCTGTGTTGTGCAAAATGCCATTGAAAGTGAACATCCCCAGGGAG  
CTGGTTGGTGGCCTGGAGCTTCCCTGACCAACACCTCTGCCAGGAGTGTCCAACGGCACCCATGTCAACAT  
CCTCTCTCTCAAGACATGTGGTACAGTGGTCACTGTGGTAATGACAAGATTGTGCCAGCACCTCGTGA  
CAGGTCTACCCAAGCAGACCCGGGGAGCAGCGGGACTTCATCATCGAACAGCAAGCTGCTGATCCCCGT  
ACCTGCGAGTTCCACGCCGTGACACCATTCTGAAGGATACGTTCCAAACCTTCGAAACTCCCCACTGGAAAT  
CATGAGCCGAAATCATGGGATCTCCCAATTCACTCTGGAGATCTCAAGGACAATGAGTTGAAGAGCCTTAC  
GGGAAGCTCTGCCACCCCTCAAGCTCGTGAECTCCCTACTTGGCATGGCCCTGGTGCAGTGAGCG  
TTGGAAAGCTTGGTGGAGAGCTGCTTGGCACCACCCACCTCCAGATCGACGAGGTCTGAAATACTACCTCAT  
CCGGGATGGCTGTGTTCAAGATGACTCGTAAGCAGTACACATCCGGATCACCTAGCAAAGCACTTCCAGG  
TCCCTGCTTCAAGTTGTGGCAAAGACCACAAGGAAGTGTCTGCACTGCCGGTTCTGTGTGGAGTG  
TTGGACGAGCGTCCCGCTGTGCCACGGGTTGCCACCGGCAATGCCGTGCTGGGAGGAGACTCAGC  
CGGTCTACAGGCCAGCGCTAACAGGCCGGGATCCGCACTGACTGGGAGGACTAGTCGTAGCCATACCTC  
GAGTCCCTGCATTGGACGGCTCTGCTCTGGAGCTCTCCCCACCGCCCTCAAGAACATCTGCCAACAGC  
TGGGTTCAAGACTTCACACTGTGAGTCAGACTCCAGCACCAACTCACTCTGATTCTGCTCATTCACTGGCA  
CAGGTCAAGCACTGCTGAACAATGTCGGCTGGGGTTCATCTTCTAGGGTTGAAAACACTAAACTGTCCA  
CCCAGAAAGACACTCACCCATTCCCTCATTTCTTCACTACTAAACACTGTGTATGGTGCAATCAGAC  
CACAAATCAGAAGCTGGGTATAATTTCAAGTACAAACCTAGAAAATTAACAGTTACTGAAATTATGA  
CTTAAATACCAATGACTCCTTAAATATGTAATTAGTTACCTTGAAATTCAATTCAAATGCAGACTAA  
TTATAGGAATTGGAAAGTGTATCAATAAACAGTATATAATT

## **FIGURE 110**

MPPFLLITCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFTGMAGDAMP  
TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCILWNTTVEVKACPGGYYVRLTKPSVCFHV  
YCGHFYDICDEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV  
LRSDGKTCEDVEGCHNNNGGCSHSLGSEKGYQCECPRLVLSEDNHTCQVPVLCKSNAIEVNIPRELVGG  
LELFILTNTSCRGVSNGTHVNILFSLKTCGTVVDDVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT  
CEFPRLYTISEGYVPNLRNSPLEIMSRNHGIFPFITLEIFKDNEFEEPYREALPTLKLRSLSYFGIEPVVHV  
SGLESLVESCFAATPTSKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFVGKDHKEVFLHCRV  
LVCGVLDERSRCAQGCHRRMRRGAGGEDSAGLQGQTLTGGPIRIDWED

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

**Tyrosine kinase phosphorylation sites.**

amino acids 411-418, 443-451

**N-myristoylation sites.**

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
522-528, 531-537

**Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

**ZP domain proteins.**

amino acids 431-457

**Calcium-binding EGF-like proteins.**

amino acids 191-212, 232-253

## **FIGURE 111**

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG  
GCCCTCCAGCCAGTGTGACCAGGGACTTCTGACCTGCTGCCAGCCAGGACCTGTGTGGGAGGCC  
CCTGCTGCCCTGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT  
TACAGGATCCTGACAGTGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGAAACCCGTATCCCC  
ATGGAGACCTTCAGAAAGGTGGGATCCCCATCATCATAGCACTACTGAGGCTGGCAGTATCATCATTGT  
GGTTGTCCCTCATCAAGGTGATTCTGGATAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCGA  
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC  
CCCAGGGCCTGCAGTGGCAGTCGGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC  
AGGGAACGGTTCTCGCTGTTGACAACCTCACAGAACGCTCGCTGAGACAGCCTGTAGGCAGATGG  
GCTACAGCAGAGCTGTGGAGATTGCCAGACCAAGGATCTGGATGTTGTTGAAATCACAGAAAAGCCAG  
GAGCTTCGCATGCGGAACATCAAGTGGCCCTGTCAGGCTCCCTGGCTCCCTGCACGTCTGCCTG  
TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGGAGGAGGCTCTGGATTCTGGCTTGGCAGG  
TCAGCATCCAGTACGACAAACAGCACGTCTGGAGGGAGCATCCTGGACCCCCACTGGTCCTCACGGCA  
GCCCACTGCTTCAGGAAACATACCGATGTGTTCACTGGAAAGGTGGGGCAGGCTCAGACAAACTGGCAG  
CTTCCCACCCCTGGCTGTGGCAAGATCATCATCATTGAATTCAACCCATGTACCCCCAAAGACAATGACA  
TCGCCCTCATGAAGCTGCAGTCCCACTCACTTCTCAGGCACAGTCAGGCCATCTGTCTGCCCTCTT  
GATGAGGAGCTCACTCCAGCCACCCACTCTGGATCATTGGATGGGTTACGAAGCAGAATGGAGGGAA  
GATGTCGACATACTGCTGCAGGCGTCAGTCCAGGTATTGACAGCACACGGTGCAATGCAGACGATGCGT  
ACCAGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGTGTGGACACCTGCCAGGGT  
GACAGTGGTGGGCCCTGATGTACCAATCTGACCGATGGCATGTGGTGGCATCGTTAGCTGGGCTATGG  
CTGGGGGGGCCGAGCACCCCAGGAGTATACACCAAGGTCTAGCCTATCTCAACTGGATCTACAATGTCT  
GGAAGGCTGAGCTGTAATGCTGCTGCCCTTGCAGTGTGGAGCCCTTCCCTGCCCTGCCACCT  
GGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCTGGTACACCCCTGCCCACAGCCTAGCAT  
TTCTGGAGCAGCAAAGGCCCTCAATTCTGTAAGAGACCCCTCGCAGCCAGAGGCGCCAGAGGAAGTCA  
GCAGCCCTAGCTCGGCCACACTGGTGCTCCAGCATCCCAGGGAGAGACACAGCCCACGTAAACAAGGTCT  
CAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACACTGAATGGAAGCAGGCTGTCTTGAAAGCC  
CAGATCACTGTGGCTGGAGAGGAGAAGGAAAGGGTCTGCCAGCCCTGCGTCTTCAACCCATCCCCAA  
GCCTACTAGAGCAAGAACCAAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT  
ACTGTTGTCATTGTTATTACAGCTATGCCACTATTATAAGAGCTGTGTAACATCTGGCAAAAAAAA  
AAAA

## **FIGURE 112**

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIALLSLASIIIVVVLIKVILDKYFLCG  
QPLHFI PRKQLCDGELDCPLGEDEEHCVKS FPEGPAVAVRLSKDRSTLQVLD SATGNWFSACFDN  
FTEALAE TACRQM GYSRAVE IGP DQD L DV EITEN SQEL RMRN SSGP CLSGS LVSLHCLACG KSL  
KTPR VVGGEE ASVDSWPWQVS IQYDKQHV CGGS ILDPHW VLTA AHCF RKHTD VFNWKVRAGSDKL  
GSFPSL AVAK III IFNP MYPKDNDI ALMKLQFPLTFS GTVRPICL PFFDEELTPATPLWIIIGWG  
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDT CQGD SGGPLMYQS  
DQWHVVGIVSWGYGC GG P STPGVYTKVSAYLNWIYNVWK AEL

**Transmembrane domain:**

amino acids 32-53 (type II)

## **FIGURE 113**

GGCTGGACTGGAACCTGGTCCAAGTGATCCACCCGCCTCAGCCTCCAAAGGTGCTGTGATTA  
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACATTTCAGCAACTAAAAAGCCACAGGAGT  
TGAACGTCTAGGATTCTGACTTGCTGTGGCTAGTGCTCCTACTCCTACCTACATTAAAATC  
TGTTTTTGTTCTCTTGTAACTAGCCTTACCTCCTAACACAGAGGATCTGTCACTGTGGCTCT  
GGCCCAAACCTGACCTCACTCTGGAACGAGAACAGAGGTTCTACCCACACCGTCCCCTGAAG  
CCGGGGACAGCCTCACCTGCTGGCCTCTCGCTGGAGCAGTGCCCTACCAACTGTCTCACGTCT  
GGAGGCAGTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTGGTAGCTGCGGCTTCAAGGTGGC  
CTTGCCCTGGCCGTAGAAGGGATTGACAAGCCGAAGATTTCATAGGCATGGCTCCACTGCC  
AGGCATCAGCCTGCTGTAGTCATCACTGCCCTGGGCCAGGACGGCCGTGGACACCTGCTCA  
GAAGCAGTGGGTGAGACATCACGCTGCCGCCATCTAACCTTTATGTCCCTGCACATCACCTG  
ATCCATGGGCTAATCTGAACCTGTCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC  
CAGAAGGGGTCTGCTTAGACCACCTGGTTATGTGACAGGACTTGACATTCTCCTGGAACATGAGG  
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAAGGAACCTGTGCCAATTATGGGTCAAGAAAGATG  
GAGGTGTTGGTTATCACAAGGCATCGAGTCTCCTGCATTCACTGGAGCAGATGTGGGGAAAGGCTG  
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGCCATCAGACAGCGTTCCGCCCGAT  
CCACGTACCAAGCTGCTGAAGGGCAACTGCAGGCCATGCTCTCATGCCAGGCAGCAGCCAAA  
TCTGCGATCACCAGCCAGGGCAGCCGTCTGGAAAGGAGCAAGCAAAGTGACCATTCTCCTCCC  
CTCCTTCCCTCTGAGAGGCCCTCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG  
GGCTAATGGCTCAGTGTGGCCCTAGGAGGTCAGCAAGGCTGAGAGCTGATCAGAAGGGCTGCT  
GTGCGAACACGGAAATGCCCTCAGTAAGCACAGGCTGAAAATCCCAGGCAAAGGACTGTGTGG  
CTCAATTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGTT  
CAAATGATCTCCAAGGGCCTTATACCCCAGGAGACTTGTGATTGAAACCCCAAATCCA  
AACCTAAGAACCAAGGTGCATTAAGAACATCAGTTATTGCCGGGTGTGGCCTGTAATGCCAACAT  
TTGGGAGGCCAGGGCGGGTAGATCACCTGAGGTCAAGGAGCTGACAGGCCAGGCCAACATGG  
TGAAACCCCTGTCTACTAAAAAAACTAGCCAGGCATGGGGAGGTGAAGGAGGCTGAGACA  
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAAACCTGGGAGGTGAAGGAGGCTGAGACA  
GGAGAACATTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAGAATTA  
TGGTTATTGTAA

## **FIGURE 114**

MLWWLVLLLPTLKVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC  
WPLAGAVPSPTVSRLALTRAVQVAEPLGSCGFQGGPCPGRRD

**Signal peptide:**

amino acids 1-15

## **FIGURE 115**

CAGCAGTGGCTCTCAGTCCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA  
AGAATCCTCCAGAGAATTGTGAAGACTGTACATTCAAATGCAGAAGCTTTAAATCCAAGAAA  
ATATGTAATCACTTAAGATTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACCTAATTGTCT  
GTTTGGGGAGCAAGCACTCTGGCCGGAGGTACCCAAAAAGCTATGACATGGAGCACACTT  
TCTACAGCAATGGAGAGAAGAAGATTTACATGGAATTGATCCTGTGACCAGAACTGAAATA  
TTCAGAAGCGAAATGGCACTGATGAAACATTGAAAGTGCACGACTTAAACCGGATAACACTGG  
CATCTACTTCGTGGTCTCAAAATGTTTATCAAACACTCAGATTAAGTGATTCTGAATT  
CTGAACCAGAAGAGGAAATAGATGAGAATGAAAGAAATTACCAACTTTCTTGAAACAGTCAGTG  
ATTGGTCCCAGCAGAAAAGCTATTGAAAACCGAGATTCTTAAACCTGAA  
GATTGTGATAACGTGACCATGTATTGGATCAATCCCACCTAATATCAGTTCTGAGTTACAAG  
ACTTGAGGAGGAGGGAGAAGATCTCACTTCCCTGCCAACGAAAAAAAGGGATTGAAACAAAT  
GAACAGTGGTGGTCCCTCAAGTGAAGTAGAGAAGACCCGTACGCCAGACAAGCAAGTGAGGA  
AGAACTCCAATAATGACTATACTGAAAATGGAATAGAATTGATCCCATGCTGGATGAGAGAG  
GTTATTGTTGATTACTGCCGTGAGGCAACCGCTATTGCCGCCGTCTGTGAACCTTACTA  
GGCTACTACCCATATCCACTGCTACCAAGGGAGGACGAGTCATCTGCGTGTCACTGCCCTG  
TAACTGGTGGTGGCCCGATGCTGGGAGGGTCTAATAGGAGGTTGAGCTCAAATGCTAAAC  
TGCTGGCAACATATAATAATGCTATTCAATGAATTCTGCCTATGAGGCATCTGGCCCT  
GGTAGCCAGCTCTCCAGAATTACTGTAGGTAAATTCTCTCTTCATGTTCTAATAAAACTTCTACA  
TTATCACCAAAAAAAAAAAAAAA

## **FIGURE 116**

MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTLLIVLFWGSKHFWPEVPKKAYDME  
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP  
EFSEPEEEIDENEEITTFEQSVIWWPAEKPIENRDFLKNKILEICDNVTMYWINPTLISVSE  
LQDFEEEEDLHFPAEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLD  
ERGYCCIYCRRGNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWVARMLGRV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-  
242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

## **FIGURE 117**

GAGCTCCCTCAGGAGCGCGTTAGTTCACACCTCGCAGCAGGAGGGCGGCAGCTCTCGCAGGCGGA  
GGGCGGGCGGCCAGGATCATGTCCACCACCATGCCAAGTGGTGGCGTCTCTGTCCATCCTGGGCT  
GGCGGCGTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCAGGACCTGTACGACAACCCGTACCT  
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTCGTGTAGGAGAGTTCAGGCTTCACCGAATGCAGGCC  
TATTTCAACCACATCCTGGACTTCAGCCATGCTCGAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGCCT  
GGGTGCCATTGGCCTCTGGTATCCATCTTGCCCTGAAATGCATCCGATTGGCAGCATGGAGGACTCTG  
CCAAAGCCAACATGACACTGACCTCCGGGATCATGTTCAATTGTCTCAGGCTTGTGCAATTGCTGGAGTG  
TCTGTGTTGCCAACATGCTGGTACTAACTTCTGGATGTCCACAGCTAACATGTACACCGCATGGTGG  
GATGGTGCAGACTGTTCAAGACCAGGTACACATTGGTGCAGGCCCTGTTGTGGCTGGTCGCTGGAGGCC  
TCACACTAATTGGGGGTGTGATGATGTGCATGCCCTGCCGGGCTGGCACCAGAAGAAACCAACTACAAA  
GCCGTTCTTATCATGCCCTCAGGCCACAGTGGTGCCTACAAGCCTGGAGGCTCAAGGCCAGCACTGGCTT  
TGGGTCCAACACCAAAAACAAGAAGATAACGATGGAGGTGCCGCACAGAGGACGAGGTACAATTTATC  
CTTCCAAGCAGACTATGTTAATGCTCTAAGACCTCTCAGCACGGCGGAAGAAACTCCGGAGAGCTCA  
CCCCAAAAACAAGGAGATCCCACATCTAGATTCTCTGGTTGACTCACAGCTGGAGTTAGAAAAGCCT  
CGATTTCATCTTGAGAGGCCAATGGCTTAGCCTCAGTCTGTCTAAATATTCCACCATAAAACA  
GCTGAGTTATTTATGAATTAGGGCTATAGCTCACATTTCATCCTCTATTCTTTAAATATAACT  
TTCTACTCTGATGAGAGAATGTGGTTTAATCTCTCTCACATTGATGATTTAGACAGACTCCCCCTC  
TTCCTCTAGTCATAAAACCCATTGATGATCTATTCCAGCTTATCCCCAAGAAAATTGGAAAGGAAA  
GAGTAGACCCAAAGATGTTATTCTGCTGTTGAATTGTCTCCCCACCCCAACTGGCTAGTAATAA  
ACACTTACTGAAGAAGAAGCAATAAGAGAAGATAATTGTAATCTCTCCAGCCCAGTCTCGGTTTCTT  
ACACTGTGATCTAAAGTACCAAAACCAAGTCATTTCACTGGTGGAGGACCAACCTTCTACTGCTG  
TTGACATCTCTTATTACAGCAACACCATTCTAGGAGTTCTGAGCTCTCCACTGGAGTCCTTTCTGT  
CGCGGGTCAGAAAATTGCTCTAGATGAATGAGAAAATTATTTTTAATTAAAGTCTAAATATAGTTAA  
AATAAAATAATGTTAGTAAAATGATACACTATCTCTGTGAAATAGCCTACCCCTACATGTGGATAGAAG  
GAAATGAAAAATAATTGCTTTGACATTGTCTATGGTACTTGTAAAGTCATGCTTAAGTACAAATTCC  
ATGAAAAGCTCACACCTGTAATCTAGCACTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGT  
TCGAGACTAGCCTGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTC  
TGGTGGCATACACCTGTAGTCCCAGCATTCCGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGT  
TGGGGCTGCAGTGAGGCCATGATCACACCACTGCACTCCAGCAGGTGACATAGCGAGATCCTGTCTAAAAAA  
AATAAAAAATAATGAAACACAGCAAGTCCTAGGAAGTAGGTTAAAACATAATTCTTTAA

## **FIGURE 118**

MSTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTECRP  
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFIVSGL  
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA  
CRGLAPEETNYKAVSYHASGHHSVAYKPGGFCASTGFGSNTKNKKIYDGGAARTEDEVQSYP SKHDY  
V

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

## **FIGURE 119**

GGAAAAACTGTTCTCTTGTGGCACAGAGAACCCGTCTAAAGCAGAAGTAGCAGTCCGGAGTC  
AGCTGGCTAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGCTGTTCTTG  
GTGGTGTGGAATGGTGGCACAGTGGCTGCACTGTCATGCCTCAGTGGAGAGTGTGGCCTTCATT  
GAAAACAACATCGTGGTTTGAACACTCTGGAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA  
CATCAGGATGCAGTGCACAAATCTATGATTCCCTGCTGGCTTCTCCGGACCTACAGGCAGCCAGAG  
GACTGATGTGTGCTGCTCCGTGATGTCCTTCTGGCTTCATGATGCCATCCTGGCATGAAATGC  
ACCAGGTGCACGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTCAT  
CATCACGGGCATGGTGGTGCTCATCCCTGTGAGCTGGGTGCCAATGCCATCATCAGAGATTCTATA  
ACTCAATAGTGAATGTTGCCAAAAACGTGAGCTGGAGAAGCTCTACTTAGGATGGACCACGGCA  
CTGGTGCTGATTGTTGGAGGAGCTCTGTTCTGCGTTTGTGCAACGAAAAGAGCAGTAGCTA  
CAGATACTCGATACCTTCCCATCGCACAACCCAAAAAGTTATCACACCGAAAGAAGTCACCGAGCG  
TCTACTCCAGAAGTCAGTATGTTAGTTGTATGTTTAACTTACTATAAGCCATGCAAATG  
ACAAAAATCTATATTACTTCTCAAAATGGACCCCCAAAGAAACTTGATTACTGTTCTTAACGCCT  
AACTTAAATTACAGGAACGTGCATCAGCTATTATGATTCTATAAGCTATTCAAGCAGAATGAGATA  
TTAAACCCAATGCTTGATTGTTCTAGAAAGTATAGTAATTGTTCTAAGGTGGTCAAGCATTCTA  
CTCTTTTATCATTACTTCAAAATGACATTGCTAAAGACTGCATTATTACTACTGTAATTCTCC  
ACGACATAGCATTATGTACATAGATGAGTGTAAACATTATATCTCACATAGAGACATGCTTATATGGT  
TTTATTAAAATGAAATGCCAGTCCATTACACTGAATAATAGAACTCAACTATTGCTTTCAGGGAA  
ATCATGGATAGGGTTGAAGAAGGTTACTATTAAATTGTTAAAACAGCTAGGGATAATGCTTCC  
TTTATAATGAAGATAAAATGAAGGCTTAATCAGCATTGTAAGAAAATTGAATGGCTTCTGATAT  
GCTGTTTTAGCCTAGGAGTTAGAAATCTAACTCTTATCCTCTTCTCCAGAGGCTTTTT  
CTTGTGATTAAATTAAACATTAAAACGCAGATATTGTCAGGGCTTGCATTCAAACAGCT  
TTCCAGGGCTACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAGTGTGATGGTTAGGAAAGTG  
AAAATTTTGTGTTGTATTGAAGAAGAATGATGCATTGACAAGAAATCATATATGTATGGAT  
ATATTAAATAAGTATTGAGTACAGACTTGGGTTCATCAATATAAAAGAGCAGAAAAATA  
TGTCTGGTTTCATTGCTTACCAAAAAACACAACAAAAAGTTGCTTGTGAGAACCTCACCT  
GCTCCTATGTGGTACCTGAGTCAGTAACTGTCATTGTTCTGTGAAAATAAATTCTCTGTA  
CCATTCTGTTAGTTACTAAAATCTGAAATACTGTATTGTTCTGTTATTCAAATTGATGAA  
ACTGACAATCCAATTGAAAGTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTT  
TATACATTATATAAATTGTCATTTCTAATT

## **FIGURE 120**

MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSIFIENNIVVFENFWEGLWMNCVRQANIRMQCK  
IYDSLLALSPDLQAARGLMCAASVMSFLAFMAILGMKTRCTGDNEKVKAHILLTAGIIFIITG  
MVVLIPSWVANAIIRDGYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY  
RYSIPSHRTTQKSYHTGKKSPSVRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

## **FIGURE 121**

GGAGAGAGGCGCGCGGGTGAAGGCGCATTGATGCAGCCTCGGGCGCCTCGGAGCGCGGGAG  
CCAGACGCTGACCACGTTCCCTCCTCGGTCTCCGCCCTCCAGCTCCCGCTGCCGGCAGCC  
GGGAGCCATGCGACCCCAGGGCCCCGCGCCTCCCGCAGCGGCTCOGCGGCCTCCTGCTGCTCC  
TGCTGCTGAGCTGCCCGCGCCGTGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCCAG  
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC  
TGGTCGAGACGGGAGCCCTGGGCCAATGTTATTCCGGTACACCTGGATCCCAGGTGGATG  
GATTCAAAGGAGAAAAGGGGAATGTCAGGGAAAGCTTGAGGAGTCTGGACACCCAAC  
AAGCAGTGGTCATGGAGTTCAATTGCAATTGGCATAGATCTGGAAAATTGCGGAGTGTACATT  
TACAAAGATGCGTTCAAATAGTGTCTAACAGAGTTGTTCAAGTGCTCACTCGGCTAAAATGCA  
GAAATGCATGCTGTCAGCGTTGGTATTCACATTCAATGGAGCTGAATGTTCAAGGACCTCT  
ATTGAAGCTATAATTATTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAAATT  
CATCG CACTCTCTGTGAAAGGACTTGTGAAGGAATTGGTGGCTGGATTAGTGGATGTTGCTATCT  
TTGGCAGTGGTCAGATTACCAAAAGGAGATGCTTCACTGGATGGAATTCAAGTTCTCGC  
ATTATTGAAGAACTACCAAAATGCTTAATTTCATTGCTACCTCTTTTTATTATGCC  
TTGGAATGGTTCACTTAAATGACATTAAATAAGTTATGTATAACATCTGAATGAAAAGCAA  
CTAAATATGTTACAGACCAAAAGTGTGATTCAACTGTTAAATCTAGCATTATT  
CTTCACAACTATAATTGGAATTGTTGGCTTTCTCTTAGTATAGCATT  
AAAAAAATAAAAAGCTACCAATCTTGTACAATTGTAAGAATT  
TAAATAAAAATTATTCCAACA

## **FIGURE 122**

MRPQGPAAASPQRRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGR  
DGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK  
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMNSTINIHRTS  
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

## **FIGURE 123**

GCTGAGCGTGTGCGCGTACGGGCTCTCTGCCTCTGGCTCCAACGCAGCTGTGGCTGAA  
CTGGGTGCTCATCACGGAACTGCTGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA  
ATTGCCTGGAAGAATACATCATGTTTCGATAAGAAGAAATTGTAAGGATCCAGTTTTTTTA  
ACCGCCCCCTCCCACCCCCAAAAAAACTGTAAGATGCAAAAAGTAATATCATGAAGATCC  
TATTACCTAGGAAGATTTGATTTGCTGCGAATGCCGTGTTGGATTATTGTTCTGGAG  
TGTTCTGCGTGGCTGCAAAGAATAATGTTCAAATCGTCCATCTCCCAAGGGGTCCAATT  
TCTTCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGGCTGTCATGCAACTG  
GCCCTAAGCCAAAGCAGGACCTAAGGACGACCTTGAACAATACAAGGATGGGTTCAATG  
TAATTAGGCTACTGAGCGGATCAGCTGAGCACTGGTTATAGCCCCACTGTCTACTGACAATG  
CTTTCTCTGCCGAACGAGGATGCCCTAAGGGCTGAGGTGTAAGGCAAATGGTATATTGTA  
ATCTCAGAAATTACAGGAGATCCCTCAAGTATATCTGCTGGTGTAGGTTGCTCCCTCGCT  
ATAACAGCCTTCAAAAATTAAAGTATAATCAATTAAAGGGCTCAACAGCTCACCTGGCTATAC  
CTTGACCATAACCATATTGACGAAAATGCTTTAATGGAATACGCAAGCTCAAAGA  
GCTGATTCTTAGTCCAATAGAATCTCTTCTTCTTAAACAAACCTTCAGACCTGTGACAATT  
TACGGAACTTGGATCTGCTTATAATCAGCTGCATTCTGGGATCTGAACAGTTTGGGCTTG  
CGGAAGCTGCTGAGTTTACATTACGGCTAACCTGGAGCTTACAAAGGCTTGAAGGAAATTC  
AGACTGCCGAACCTGGAACCTTGGACCTGGGATATAACGGGATCAGAAGTTAGCCAGGAATG  
TCTTGCTGGCATGATCAGACTCAAAGAACCTCACCTGGAGCACAATCAATTTCAGCTCAC  
CTGGCCCTTTTCAAGGTTGGTCAGCCTTCAGAACCTTACTTGCACTGGAAATAATCAGTGT  
CATAGGACAGACCATGTCTGGACCTGGAGCTCTTACAAAGGCTTGAATTATCAGGCAATGAGA  
TCGAAGCTTCAGTGGACCCAGTGTGTTTCCAGTGTGTCCGAATCTGCAGCGCCCTCAACCTGGAT  
TCCAACAAGCTCACATTATTGGTCAAGAGATTGGATTCTGGATATCCCTCAATGACATCAG  
TCTTGCTGGGAATATGGGAATGCAAGAACATATTGCTCCCTGTAAACTGGTGAAGATT  
TTAAAGGTCTAAGGGAGAATACAATTATCTGTCAGTCCAAAGAGCTGCAAGGAGATAATGTG  
ATCGATGCAGTGAAGAACTACAGCATCTGGCAAAAGTACTACAGAGAGGTTGATCTGGCAG  
GGCTCTCCAAAGCCGACGTTAACGCAAGCTCCCCAGGCCAGACATGAGAGCAACCCCT  
TGCCCCCGACGGTGGGAGCCACAGAGCCCCCAGAGACCGATGCTGACGCCAGCACATCT  
TTCCATAAAATCATCGCGGGCAGCGTGGCCTTCTGTGTCGTGTCATCCGTGGTT  
CTACGTGTCATGGAAGCGGTACCTGCGAGCATGAAGCAGCTGCAAGCGCTCCCTCATGCGA  
GGCACAGGAAAAGAAAAGACAGTCCCTAACGAAATGACTCCCAGCACCCAGGAATTATGTA  
GATTATAAACCCACCAACACGGAGACCGAGATGCTGTAATGGGACGGGACCCCTGCACCTA  
TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACTCTGGTACTATCAAGGGAACCGGATGCC  
GGGAAATAAGTGGTCTTATTGAACTCTGGTACTATCAAGGGAACCGGATGCCCTCC  
TTCCCTCTCCCTCACTTGGTGGCAAGATCCTCCTGTCCGTTAGTGCATTATAACT  
GGTCATTTCCTCTACATAATCAACCCATTGAAATTAAATACCAATCAATGTGAAGCTT  
GAACTCCGGTTAATATAATACCTATTGTATAAGACCCCTTACTGATTCCATTATGTCGCA  
GTTTAAGATAAAACTTCTTCATAGGAAAAAAAAAA

## **FIGURE 124**

MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGKMYCSESQKLQEIPSSISAGCLG  
LSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYFLNNTR  
PVTNLRNLDLSYNQHLHSLGSEQFRGLRKLLSLHRSNSLRTIPVRIQDCRNLELLDLGYNRIRS  
LARNVFAGMIRLKELHLEHNQFSKLNLALFPRLVSLQNLQWNKISVIGQTMSTWSSLQRDL  
SGNEIEAFSGPSVFQCVPNLQRLNLDNSNKLTFIGQEILDWSISLNDISLAGNIWECSRNICSLVN  
WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE  
SKPPLPPTVGATEPGPETDADAEHISFHKIAGSVALFLSVLVILLVIYVSWKRYPASMKQLQQR  
SLMRRHRKKKRQSLQMTSTQEFYVDYKPTNTETSEMLLNGBTGPCTYNKSGSRECEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

## **FIGURE 125**

CCGTTATCGTCTTCGCTACTGCTGAATGTCCGTCCCAGGAGGAGGGCTTTGCCGCTG  
ACCCAGAGATGGCCCCGAGCGAGCAAATTCTACTGTCCGGCTGCCGCGTACCGTGGCCGAGCT  
AGCAACCTTCCCTGGATCTCACAAAAACTCGACTCCAATGCAAGGAGAACGAGCTTGCTC  
GGTGGGAGACGGTGCAGAGAATCTGCCCTATAGGGGAATGGTGCACAGCCCTAGGGATC  
ATTGAAGAGGAAGGCTTCTAAAGCTTGGCAAGGAGTGACACCCGCCATTACAGACACGTAGT  
GTATTCTGGAGGTGCAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTGGCAAAAGTGAAG  
ATGAGCATTATCCCCCTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCAGTT  
TTAGCCAATCCAAC TGACCTAGTGAAGGTTAGATGCAAATGGAAGGAAAAGGAACTGGAAGG  
AAAACCATTGCGATTCGTGGTGTACATCATGCATTGCAAAATCTAGCTGAAGGAGGAATAC  
GAGGGCTTGGGCAGGCTGGTACCCAATATACAAAGAGCAGCACTGGTAATATGGGAGATTAA  
ACCACTTATGATACTGAAACACTACTTGGTATTGAATACACCACCTGAGGACAATATCATGAC  
TCACGGTTATCAAGTTATGTTCTGGACTGGTAGCTCTATTCTGGAACACCAGCCATGTCA  
TCAAAAGCAGATAATGAATCAACCACGAGATAAACAGGAAGGGACTTTGTATAAATCATCG  
ACTGACTGCTTGATTCAAGGCTGTTCAAGGTGAAGGATTGAGTCTATATAAAGGCTTTTACC  
ATCTTGGCTGAGAATGACCCCTGGTCAATGGTGTGTTCTGGCTTACTTATGAAAAAAATCAGAGAGA  
TGAGTGGAGTCAGTCCATTTAA

## **FIGURE 126**

MSVPPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGARES  
APYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVSGGRMVTYEHLREVVFGKSEDEHYPLWKS  
VIGGMMAGVIGQFLANPTDLVKVQMOMEGRKRKLEGKPLRFRGVHAFAKILAEGGIRGLWAGWVP  
NIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTPADVIKSRI MNQP  
RDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

## **FIGURE 127**

CGCGGATCGGACCAAGCAGGT CGGC GGCG CAGGAGAGCGGCCGGCGTCAGCTCCTCGAC  
CCCCGTGTCGGCTAGTCCAGCGAGGCGACGGCGGTGGGCCATGGCCAGGCCGGCATGG  
AGCGGTGGCGCACGGCTGGCGCTGGTGACGGGGCCTCGGGGGCATCGGCGGGCGTGGCC  
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGCGTGC GCCGCACTGTGGGCAACATCGAGGA  
GCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCGGGACTTGATCCCCTACAGATGTGACCTAT  
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATC  
TGCATCAACAATGCTGGCTTGGCCGGCTGACACCCCTGCTCTCAGGCAGCACAGCGGTGTGGAA  
GGACATGTTCAATGTAACGTGCTGGCCCTCAGCATCTGCACACGGAAAGCCTACCAGTCCATGA  
AGGAGCGGAATGTGGACGATGGGCACATCATTAAACATCAATAGCATGTCGGCACCGAGTGTAA  
CCCCGTGCTGTGACCCACTTCTATAGTGCACCAAGTATGCCGTACTGCCGTGACAGAGGGACT  
GAGGCAAGAGCTCGGGAGGCCAGACCCACATCCGAGCCACGTGCATCTCCAGGTGTGG  
AGACACAATTGCGCTTCAAACCTCCACGACAAGGACCTGAGAAGGCAGTGCACCTATGAGCAA  
ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCCTCAGCACCCCCGCACA  
CATCCAGATTGGAGACATCCAGATGAGGCCACGGAGCAGGTGACCTAGTGACTGTGGAGCTCC  
TCCTCCCTCCCCACCCCTCATGGCTGCCCTGCCTCTGGATTTAGGTGTTGATTTCTGGAT  
CACGGGATACCACTCCTGTCCACACCCCGACCAGGGCTAGAAAATTGTTGAGATTTATA  
TCATCTGTCAAATTGCTCAGTTGTAATGTAAGGGCTGGGAAAGGAGGTGGTGTCCC  
TAATTGTTTACTTGTAACTTGTCTTGCCCTGGCACTGGCCTTGTCTGCTCTCAGTG  
TCTTCCCTTGACATGGGAAAGGAGTTGTGGCCAAATCCCCATCTTGTGCACCTAACGTCTG  
TGGCTCAGGGCTGGGTGGCAGAGGGAGGCCTCACCTATATCTGTGTTATCCAGGGCTCC  
AGACTTCCTCCTGCCTGCCCTGCACCTCTCCCCCTATCTATCTCCTCTCGGCTCCCC  
AGCCCAAGTCTGGCTTGTCCCCTGGGTATCCCTCACTCTGACTCTGACTATGGCAG  
CAGAACACCAGGGCCTGGCCAGTGGATTGATCATTAAAAAGAAAAATCGAACCAA  
AAAAAAAAAA

## **FIGURE 128**

MARPGMERWRDRRLALVTGASGGIGAAVARALVQQGLKVVGCARTVGNIEELAAECKSAGYPGTLI  
PYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNVNVLALSICTR  
EAYQSMKERNVDDGHIININMSGHRVLPLSVTHFYSATKYAVTALTEGLRQEELREAQTHIRATC  
ISPGVVETQFAFKLHDKDPEKAAATYEQMCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114

## **FIGURE 129**

AAC TCTACATGGGCCTCCTGCTGCTGGTGCCTTCCTCAGGCCTCCTGCCGGTGGCCTACACCAT  
CATGTCCCTCCCACCCCTCCTTGACTGCGGGCGTTCAAGGTGCAGAGTCTCAGTTGCCCGGGAGC  
ACCTCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCAGAATTCCAGTTCTGGTTCATGC  
CAGCCTGTAAAAGGCCATGGAACTTGGGTGAATCACCGATGCCATTAAAGAGGGTTTCTGCCA  
GGATGGAATGTTAGGTCGTTCTGTCTGCGCTGTTCAATTCAAGTAGCCACCAGCCACCTGTGG  
CCGTTGAGTGCTGAAATGAGGAACTGAGAAAATTAAATTCTCATGTATTTCATTTATTAA  
TTAATTAACTGATAGTTGACATATTGGGGTACATGTGATATTGGATACTGTATA  
TATATAATGATCAAATCAGGGTAACGGGATATCCATCACATCAAACATTATTTTATTCTTT  
TTAGACAGAGTCTCACTCTGTACCCAGGCTGGAGTGCAGTGGTGCATCTCAGCTTACTGCAAC  
CTCTGCCTGCCAGGTCAAGCGATTCTCATGCCCTCACCTCCAAAGTAGCTGGACTACAGGCAT  
GCACCACAATGCCCAACTAATTGTATTAGTAGAGACGGGTTTGCCATGTTGCCAGG  
CTGGCCTGAACCTGGCCTCAAACAATCCACTGCCCTGGCCTCCAAAGTGTATGATTACA  
GGCGTGAGCCACCGTGCCTGGCTAAACATTATCTTCTTGTGTTGGAACTTGA  
ACAATGAATTATTGTTAACGTCACTCCCTGCTGTGCTATGGAACACTGGGACTCTCCCTCT  
ATCTAACTGTATATTGTACCAAGTTAACCAACCGTACTTCATCCCCACTCCTCTATCCTCCCC  
AACCTCTGATCACCTCATTCTACTCTACCTCCATGAGATCCACTTTTAGCTCCACATGTG  
AGTAAGAAAATGCAATATTGTCTTCTGCTGGCTATTCACTTAACATAATGACTCCTG  
TTCCATCCATGTTGCTGCAAATGACAGGATTTCGTTCTTAATTCAATTAAAATAACCACACATG  
GCAAAAA

## **FIGURE 130**

MGLLLLVLFSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSSLRGPRPRIPVLVSCQPV  
KGHGTLGESPMFKRVFCQDGNVRSFCVCAVFSSHQPPVAVECLK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 86-92

**Zinc carboxypeptidases, zinc-binding region 2 signature.**

amino acids 68-79

## **FIGURE 131**

TTCTGAAGTAACGGAAGCTACCTGTATAAAGACCTAACACTGCTGACCATGATCAGCGCAGCCTGGAGC  
ATCTTCCTCATCGGACTAAAATTGGCTGTTCCCTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG  
TCCATCTGTGTGCGCTGCGATGCCGGTTCTACCTGAAACAAACCAAATAATGCTGGATTCCCTCAGAT  
GAATACCAAGAGGATGCTACAACTCTACCCAGAACAACCAAATAATGCTGGATTCCCTCAGAT  
TTGAAAAACTTGCTGAAAGTAGAAAGAATATACTTACCCACAACAGTTAGATGAATTTCCTACCAACCT  
CCCAAAGTATGTAAAAGAGTTACATTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTCAA  
AAATTCCCTATCTGAAAGAATTACATTTAGATGACAACACTGCTCTGCGATTAGCATAGAAGAGGGAGCA  
TTCCGAGACAGCAACTATCTCCGACTGCTTTCCGTCCCGTAATCACCTTAGCACAATTCCCTGGGGTT  
GCCAGGACTATAGAAGAACTACGCTGGATGATAATCGCATATCCACTATTCATCACCCTCTTCAAAG  
GTCTCACTAGTCTAAACGCCTGGTCTAGATGGAAACCTGTTGAACAATCATGGTTAGGTGACAAGATT  
TTCTTCACACCTAGTTAATTGACAGAGCTGTCCTGGTGCAGAATTCCCTGACTGCTGCACCAAGTAAACCT  
TCCAGGCACAAACCTGAGGAAGCTTATCTCAAGATAACCACATCAATCGGGTCCCCCAAATGCTTTT  
CTTATCTAAGGAGCTCTATCGACTGGATATGTCATAAACTTAAGTAAATTACCTCAGGGTATCTT  
GATGATTGGACAATATAACACAACTGATTCTCGCAACAACTCCCTGGTATTGGGGTGCAAGATGAAATG  
GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGCTCATGTGCCAAGCCCCAGAAA  
AGGTTCGTGGGATGGCTATTAGGATCTCAATGCAAGAACTGTTGATTGTAAGGACAGTGGGATTGTAAGC  
ACCATTACAGATAACCAACTGCAATACCAACACAGTGTATCCTGCCAAGGACAGTGGCCAGCTCCAGTGAC  
CAAACAGCCAGATAAGAACCCCAAGCTCAACTAAGGATCAACAAACACAGGGAGTCCCTCAAGAAAAAA  
CAATTACAATTACTGTGAAGTCTGACCTCTGATACCATTCTATCTCTGGAAACTGCTCTACCTATG  
ACTGCTTGAGACTCAGCTGGCTAAACTGGGCCATAGCCGGCATTTGGATCTATAACAGAAACAATTGT  
AACAGGGAAACGCACTGAGTACTGGTCACAGCCCTGGAGGCTGATTCCCTATAAAGTATGCATGGTTC  
CCATGGAAACAGCAACCTCTACCTATTGATGAAACTCCTGTTGATTGAGACTGAAACTGCACCCCT  
CGAATGTACAACCCCTACAACCAACCCCTCAATCGAGAGCAAGAGAAACCTTACAAAAACCCCAATTAC  
TTGGCTGCCATCTGGTGGGGCTGTCCTGGTACCATGGCTTCTGCTTACTGTTGATGTTGATG  
TTCATAGGAATGGATCGCTTCTCAAGGAACTGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT  
GCAGAAGCTGGCACTAAGAAGGACAACACTCTATCCTGGAAATCAGGGAAACTCTTCAAGATGTTACCAAT  
AAGCAATGAACCCATCTCGAAGGAGGAGTTGTAATACACCCATATTCCCTCTAATGGAATGAATCTGT  
ACAAAAACAATCACAGTGAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC  
TCACACTCATGATGCTGAAAGGACTCACAGCAGACTTGTGTTGGTTTTAAACCTAAGGGAGGTGATG  
GT

## **FIGURE 132**

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTLYL  
QNNQINNAGIPSIDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKIPYL  
EELHLDNSVSAVIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL  
QGLTSIKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQDNHIN  
RVPPNAFSYLRQLYRLDMSNNNLSNLQPQIFDDLDNITQLILRNNPWYCGCKMKWVRDWLQSLPV  
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDGSIVSTIQITTAIPNTVYPQAQGQWPAPVTKQPD  
IKNPKLTKDQQTGSPSRKTITITVKSVTSDTIHISWKLALPMTAIRLSWLKGHSPAFGSITET  
IVTGERSEYLVTALEPDSPYKVCMPMETSNLYLFDETPVCIETETAPLRMYNPTTLNREQEKE  
PYKNPNLPLAATIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSKGRRKDYYAEAGTKKDNS  
ILEIRETSFQMLPISNEPISKEEVVIHTIFPPNGMNLYKNNHSESSSNRSYRDSGIPDSDHSHS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 531-552

**N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

**Tyrosine kinase phosphorylation site.**

amino acids 515-522

**N-myristoylation sites.**

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,  
640-645

**Amidation site.**

amino acids 567-570

**Leucine zipper pattern.**

amino acids 159-180

**Phospholipase A2 aspartic acid active site.**

amino acids 34-44

### **FIGURE 133**

CCGTCATCCCCCTGCAGCCACCCCTCCCAGAGTCCTTGCCCAGGCCACCCAGGCTTCTGGCA  
GCCCTGCCGGGCCACTGTCTTCATGTCTGCCAGGGGAGGTGGAAAGGAGGTGGGAGGAGGGCG  
TGCAGAGGCAGTCTGGCTTGGCCAGAGCTCAGGGTGTGAGCGTGACCAGCAGTGAGCAGAG  
GCCGGCATGGCCAGCCTGGGCTGCTCCTGCTTACTGACAGCACTGCCACCGCTGTGGT  
CCTCCTCACTGCCTGGCTGGACACTGCTGAAAGTAAAGCCACATTGCAGACCTGATCCTGTCT  
GCGCTGGAGAGAGGCCACCGTCTCCTAGAACAGAGGCTGCCTGAAATCACCTGGATGGCATGGT  
GGGGGTCCGAGTGTGGAAGAGCAGCTAAAAGTGTCCGGAGAAGTGGGCCAGGAGCCCCCTGC  
TGCAGCCGCTGAGCCTGCGCTGGGATGCTGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC  
CTCCACTACCTCAAGCTGAGTGATCCAAAGTACCTAAGAGAGTTCCAGCTGACCCCTCCAGCCCCGG  
GTTTGGAAAGCTCCACATGCCTGGATCCACACTGATGCCTCCTGGTGTACCCACGTTGGGCG  
CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCCTGGTGCAGCTGCTGGAACCGGGACG  
GACAGCAGCGAGCCCTGCCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCGGCTGCTC  
AGGCTACTGCCTGTCACCAACTGCTCTTCTTCTGGCCAGAATGAGGGATGCACACAGG  
GACCACCTCAACAGAGCCAGGACTATATCACACCTCTGCGCCAACATGATGGACTTGAACCGC  
AGAGCTGAGGCCATCGGATACGCCAACCTACCCGGACATCTCATGGAAAACATCATGTTCTG  
TGGAAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA  
AACAGCAGGAAGGATGCTCGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA  
TATCAGCAGCATTTCGAGGGAGGTGAAGAGGGAGAAAAAACATTCCAGATTCTGCTCTGT  
TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTACTGCAACCTTGCCTGGGTTCAAGC  
AATTCTTGCCTCATCCTCCCGAGTAGCTGGACTACAGGAGCGTGCCACCATACCTGGCTAAT  
TTTATTTTTAGTAGAGACAGGGTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT  
CTCAAGAGATCCGCCACCTCAGGCTCCAAAGTGTGGATTTAGGTGTGAGCCACCGTGTCTG  
GCTGAAAAGCACTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTGCCACCCAGCACTC  
ATGGGGCTCTCCCTAGATGGCTGCTCCCTCCACACAGCCACAGCAGTGGCAGCCCTGG  
GTGGCTTCCATACATCCTGGCAGAACACCCCCCAGCAAACAGAGAGCCACACCCATCCACACCG  
CCACCAACAGCAGCCGCTGAGACGGACGGTCCATGCCAGCTGCCCTGGAGGAGGAACAGACCC  
TTTAGTCCTCATCCCTAGATCCTGGAGGGCACGGATCACATCCTGGAAAGAAGGCATCTGGAGG  
ATAAGCAAAGCCACCCGACACCAATCTGGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG  
GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTCAACTGCAACTGAAAAA

## **FIGURE 134**

MSARGRWEGGRRACRGSILGLARAQGAERTSSEQRPMASLGLLLLLTLAPPLWSSSLPGLD  
TAESKATIADLILSALERATVLEQRLPEINLDGMGVVRVLEEQLKSVREKWAQEPLLQPLSLRV  
GMLGEKLEAAIQRSLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE  
RSDVCLVQLLGTGTDSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQQSQD  
YINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILSWQKQQEGCFG  
EPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFKQFSCLILP  
SSWDYRSVPYLANFYIFLVETGFHHVAHAGLELLISRDPPTSGSQSVGL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 39-56

**Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

**N-myristoylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

**Amidation site.**

amino acids 10-14

**Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

### **FIGURE 135**

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTCTTCCCCTGCTGCTG  
CTGCTGCTATCGGGGATGTCCAGAGCTGGAGGTGCCGGGCTGCTGCTGAGGGATCGGAGG  
GAGTGGGGTCGGCATAGGAGATCGCTCAAGATTGAGGGCGTGCAGTTGTTCCAGGGTGAAAGC  
CTCAGGACTGGATCTGGCGCCCGAGTGTGGTAGACGGAGAAGAGCACGTCGGTTCTTAAG  
ACAGATGGAGTTTGTGGTTCATGATATACTTCTGGATCTTATGTAGTGGAGTTGTATCTCC  
AGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTCGAAAGGAAAATGAGAGCAAGATATG  
TGAATTACATCAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCAAATGAAATCTCAGGT  
CCACCTCTTACTTTATTAAAAGGGAATCGTGGGCTGGACAGACTTCTAATGAACCCAATGGT  
TATGATGATGGTTCTCCTTATTGATATTGTGCTTCTGCCTAAAGTGGTCAACACAAGTGATC  
CTGACATGAGACGGAAATGGAGCAGTCATGAATATGCTGAATTCAAACCATGAGTTGCCTGAT  
GTTCTGAGTTCATGACAAGACTCTCTCTCAAATCATCTGGCAAATCTAGCAGCGGCAGCAG  
TAAAACAGGCAAAAGTGGGCTGGCAAAAGGAGGTAGTCAGGCCGCCAGAGCTGGCATTGAC  
AAACACGGCAACACTGGTGGCATCAAAGTCTGGAAAACCGTGTGAAGCAACTACTATAAACTT  
GAGTCATCCCGACGTTGATCTCTTACAACGTGTATGTT  
AACTTTTAGCACATGTTTGTACTTGGTACACGAGAAAACCCAGCTTCATCTTTGTCTGTAT  
GAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAATTAT  
ATGAACTACTATAACATTATGTATTTAATTAAAACATCTTAATCCAGAAATCAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 136**

MAAALWGFFPVLLLLLSDVQSSSEVPGAAEGSGGSGVGIGDRFKIEGRAVPGVKPQDWISAA  
RVLVDGEHVGFLLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRARYVNVIKTSE  
VVRLPYPLQMKSSTGPPSYFIKRESWGWTDFLMNPVMVMMVLPLLIFVLLPKVVNTSDPDMRREME  
QSMNMLNSNHELPDVSEFMTRILFSSKSSGKSSGSSKTGKGAGKRR

**Important features of the protein:**

**Signal sequence:**

amino acids 1-23

**Transmembrane domain:**

amino acids 161-182

**N-glycosylation site.**

amino acids 184-187

**Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

**N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

**Amidation site.**

amino acids 238-241

**ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236

## **FIGURE 137**

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTCTCCCCAGTTCCCTGTGGGTCTGAGGGGA  
CCAGAAGGGTGAGCTACGTTGGCTTCTGGAAGGGAGGCTATATGCGTCAATTCCCCAAACAA  
GTTTGACATTCCCCTGAAATGTCATTCTATCTATTCACTGCAAGTGCGCTGCTGTTCCAGGC  
CTTACCTGCTGGCACTAACGGCGGAGCCAGGATGGGGACAGAAATAAAGGAGCCACGACCTGTGC  
CACCAACTCGCACTCAGACTCTGAACCTGAAATCTTCTCTCACGGGAGGCTGGCAGT  
TTTCTTACTCCTGTGGTCTCCAGATTCAGGCCAAGATGAAAGCCTCTAGTCTTGCCTTCAGC  
CTTCTCTGCTGCGTTTATCCTATGGACTCCTCCACTGGACTGAAGACACTCAATTGGG  
AAGCTGTGTGATGCCACAAACCTCAGGAAATACGAAATGGATTTCTGAGATACGGGGCAGTG  
TGCAAGCCAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTGCAAGACACA  
AAGCCTGCGAATCGATGCTGCCCTGCCATTGCTAAGACTCTATCTGGACAGGGTATTAA  
AAACTACCAGACCCCTGACCATTATACTCTCGGAAGATCAGCAGCCTGCCATTCTTCTTA  
CCATCAAGAAGGACCTCCGGCTCTCATGCCACATGACATGCCATTGTGGGAGGAAGCAATG  
AAGAAAATACGCCAGATTCTGAGTCACTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGC  
TTTGGGGAACTAGACATTCTCTGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTG  
CTGCTAAGAATATTGAGGTCAAGAGCTCCAGTCTCAATACCTGCAGAGGAGGCATGCCCAA  
ACCACCATCTTTACTGTACTAGTCTTGTGCTGGTCAAGTGTATCTTATTTATGCATTACTTG  
CTTCCTGCAATGGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTGTATAAGATTT  
TGTAATATCTTCTGCTATTGGATATATTATTAGTTAATATATTATTTATTTTGCTATT  
ATGTATTATTTTACTTGGACATGAAACTTTAAAAAAATTACAGATTATTTATAACCTG  
ACTAGAGCAGGTGATGTATTTTATACAGTAAAAAAAAACCTGTAAATTCTAGAAGAGTGG  
CTAGGGGGTTATTCAACTAAGGACATTTACTCATGCTGATGCTCTGTGAGAT  
ATTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTGATGTGAAATTGCAC  
ATCTACCTTACAATTACTGACCACCCAGTAGACTCCCCAGTCCCATAATTGTATCTCCAG  
CCAGGAATCCTACACGGCCAGCATGTATTCTACAAATAAGTTTCTTGCATACCAAAAAAAA  
AAAAAAAAAAA

## **FIGURE 138**

MRQFPKTSFDISPMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRPEIF  
SSREAWQFFLLLWSPDFRPKMASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG  
FSEIRGSVQAKDGNIDIRILRRTESLQDTK PANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS  
SLANSFLTIKKDLRLSHAHMTCHC GEEAMKKYSQILSHFEKLEPQA AVVKALGELDILLQWMEET  
E

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

## **FIGURE 139**

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGGAGGGCTCCAGGTGGGTCGGTCCGCATCCAGCC  
TAGCGTGTCCACGATGCGGCTGGCTCCGGACTTCGCTACCTGTTGCGTAGCGATCGAGGTGC  
TAGGGATCGCGGTCTTCCTCGGGATTCTCCCGGCTCCCGTCTGCCAGAGCGGAA  
CACGGAGCGGAGCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGTTCAACTGGACCACGCTGCC  
ACCACCTCTTCAGTAAAGTGTATTGTTCTGATAGATGCCCTGAGAGATGATTGTGTTG  
GGTCAAAGGGTGTGAAATTATGCCCTACACAACCTTACCTGTGGAAAAGGAGCATCTCACAGT  
TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCCTCGAATCAAGGCATTGATGACGGGGAG  
CCTTCCTGGCTTGTGACGTCATCAGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGA  
TAAGACAAGCAAAGCAGCTGGAAAAAGAATAGTCTTTATGGAGATGAAACCTGGGTTAAATTA  
TTCCCAAAGCATTGTGGAATATGATGGAAACAACCTCATTTCTGTCAGATTAACACAGAGGT  
GGATAATAATGTACGAGGCATTGGATAAAGTATTAAAAAGAGGAGATTGGACATATTAAATCC  
TCCACTACCTGGGGCTGGACCACATTGGCACATTTCAGGGCCCAACAGCCCCCTGATTGGCAG  
AAGCTGAGCGAGATGGACAGCGTGCTGATGAGATCCACACCTCACTGCACTGCAAGGAGAGA  
GACGCCCTAACCAATTGCTGTTCTTGTGGTACCATGGCATGCTGAAAAGGAAGTCACG  
GGGCCTCCTCCACCGAGGGAGGTGAATACACCTCTGATTAAATCAGTTCTGCGTTGAAAGGAAA  
CCCGGTGATATCCGACATC~~AAAGCACG~~TGCAATAGACGGATGTGGCTGCGACACTGGCAGTAGC  
ACTTGGCTTACCGATTCCAAAAGACAGCTGAGGTGAGGAGCCTCTTCCAGTTGTGGAAGGAAGAC  
CAATGAGAGAGCAGTTGAGATTTCATACAGTCAGCTTAGTAAACTGTTGCAAG  
AATGTGCCGTATGAAAAAGATCTGGTTGAGCAGTTAAATGTCAGAAAGATGCA  
GAACGTGATCAGACTGTACTTGGAGGAAAGCATTGAGAAGTCCTATTCAACCTGGCTCCAAGG  
TTCTCAGGCACTGGATGCTCTGCAAGACGCTGAGCTTGTCCCTGAGTGACACAAGTGGCCCAG  
TTCTCACCTGCTCTGCTCAGCGTCCCACAGGCACTGCACAGAAAAGGCTGAGCTGGAAGTCCC  
CTGTCATCTCCTGGTTCTGCTCTTATTGGTACCTGGTCTTCCGGCGTTACGT  
CATTGTTGACCTCAGCTGAAAGTCTGCTACTTCTGTCGGCTCTCGTGGCTGGCGAGGCT  
GCCTTCGTTTACCAAGACTCTGGTGAACACCTGGTGTGGCAAGTGTGGCAGTGCCCTGGAC  
AGGGGCCCTCAGGGAGGGACGTGGAGCAGCCTTACCCAGGCTCTGGGTGTCCCACACAGGTG  
TTCACATCTGCTGCTGAGTCAGATGCCCTAGTTGGAAAGCTAGGTTCTGCGACTGTTAC  
CAAGGTGATTGTAAGAGCTGGCGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGAA  
TCGGACAGCCTCCCAGCAGAGGTGTGGAGCTGAGCTGAGGGAAGAAGAGACAATCGGCCTGGA  
CACTCAGGAGGGTCAAAAGGAGACTTGGTGCACCACTCATCCTGCCACCCCCAGAACATGCAC  
GCCTCATCAGGTCCAGATTCTTCCAAGGCGACGTTCTGTTGAAATTCTTAGTCCTGGCC  
TCGGACACCTTCATTGTTAGCTGGGAGTGGTGGTGGAGGCACTGAGAAGAGAGCGGATGGTCAC  
ACTCAGATCCACAGAGGCCAGGATCAAGGACCCACTGCACTGGCAGCAGGACTGTTGGCCCC  
ACCCCAACCCCTGCACAGCCCTCATCCCTCTGGCTGAGCCGTAGAGGCCCTGTGCTGAGTGT  
CTGACCGAGACACTCACAGCTTGTCACTCAGGGCACAGGCTCTCGGAGGCCAGGATGATCTGT  
CCACGCTTGCACCTCGGGCCCATCTGGCTCATGCTCTCTCTGCTATTGAATTAGTACCTAG  
CTGCACACAGTATGTAGTTACCAAAAGAATAACGGCAATAATTGAGAAAAAAA

## **FIGURE 140**

MRLGSGTFATCCVAIEVLGIAVFLRGFFFAPVRSSARAEHGAEPPEPSAGASSNWTLPPPLF  
SKVVIVLIDALRDDVFGSKGVKFMPYTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF  
VDVIRNLNNSPALLEDSVIRQAKAAGKRIVFYGDETVVLFPKHFVEYDGTTSFVSDYTEVDNNV  
TRHLDKVLKRGDWDLILYLHYLGLDHIGHISGPNSPLIGQKLSEMDSVLMKIHTSLQSKERETPLP  
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 58-76

**N-glycosylation sites.**

amino acids 56-60, 194-198

**N-myristoylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

**Amidation site.**

amino acids 154-158

**Cell attachment sequence.**

amino acids 205-208

### **FIGURE 141**

GGCACGAGGCAAGCCTCCAGTTATCGTACGCACCTGAAAGTCTGAGAGCTACTGCCCTACA  
GAAAGTTACTAGTGCCTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGGAGTACAAC  
TCCCTATAGAAAACA<sup>T</sup>GCACCTTAAGACC<sup>A</sup>CTCACACCTTCAGAGTGAAGA<sup>C</sup>ACTTAAAC  
CCGAAGAAATT<sup>T</sup>CAGCATT<sup>T</sup>CATGACCAGGAT<sup>A</sup>CACAAAGTACTGGTCTGGACTCTGGGAATCTCAT  
AGCAGTTCCAGATAAAA<sup>T</sup>ACTACATACGCCAGAGATCTTCTTG<sup>C</sup>ATTAGCCTCATCCTTGAGCT  
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGTCTCTAAAGGGGAGTTTG<sup>T</sup>TGTCTAC  
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTCAGCTGAAGAAGGAGAA<sup>T</sup>CTGATGAAGCT  
GGCTGCCAAAAGGAATCAGCACGCCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGA  
ACATGCTGGAGTCGGCGGCTCACCCGGATGGTCATCTGCACCTCCTGCAATTGTAATGAGCCT  
GTTGGGGTACAGATAAATTGAGAACAGGAAACACATTGAATTTCATTCAACCAGTTGCAA  
AGCTGAAATGAGCCCCAGTGAGGT<sup>C</sup>AGCGATTAGGAACTGCCCAT<sup>T</sup>GAACGCC<sup>T</sup>TCCTCGCTA  
AT<sup>T</sup>TGAACTAATTGTATAAAAACACCAAA<sup>C</sup>CTGCTCACT

## **FIGURE 142**

MLLLLLEYNFPPIENNQHLKTTHTFRVKNLNPKKFSIHQDHKVLVLDGNLIAPDKNYIRPEI  
FFALASSLSSASAEGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFI  
FYRAQVGWNMLESAAHPGWFICTSCNCNEPVGVTDFENRKHIEFSFQPVCKAEMSPSEVSD

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
amino acids 33-36

**N-myristoylation site.**  
amino acids 50-55, 87-92

**Interleukin-1**  
amino acids 37-182

## **FIGURE 143**

CTAGAGAGTATAGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTAA  
TCCAGGATCCTGTCCTTCCTGTGCTCTGAGTAGTGCCTGTCAGTGTGGGGTGGAGACAAGTTG  
TCCCACAGGGCTGTCAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACCTCTGTGGG  
CACGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCACAGTCAGCACCATGCTGGCCTGCCGTGG  
AAGGGAGGTCTGTCCTGGCGCTGCTGCTGCTCTCTAGGCTCCAGATCCTGCTGATCTATGC  
CTGGCATTCCACGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA  
CAGTGGAGTTGCTGTCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGG  
CACATCTGAATTCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT  
GGGGAGAACTAGGTGTGGAAATTGAAGACGACATTGACAACGCCATTCCAAGAAAGCACAG  
AGCTGAACAATACTTCACCTGCTTCACTCAGCACCCAGGCCCTGGATGACTCAGTCAGC  
CTCCTGAACAAGACCTGCTGGAGGGATTCCACTGAGTGAACCCACTCACAGGCTTGTCCATGT  
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTCAGTGGCTGAGCAGCT  
TTGGACTTGTGTTATCCTATTTGCATGTGTTGAGATCTCAGATCAGTGTAGTTAGAAAATCC  
ACACATCTTGAGCCTAACATCATGTAGTGTAGATCATTAAACATCAGCATTAAAGAAAAAAAAAAA  
AAA

## **FIGURE 144**

MLGLPWKGGLSWALLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY  
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNNTFTCFFTISTRP  
WMTQFSLLNKTCLEGFH

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 117-121, 139-143

**N-myristoylation site.**

amino acids 9-15

## **FIGURE 145**

CTGTGCAGCTCGAGGGCTCCAGAGGCACACTCCAGAGAGGCCAAGGTTCTGACCGGATGAGGAAG  
CACCTGAGCTGGTGGCTGGCACTGTCTGCATGCTGCTTCAGCCACCTCTGCGGTCCA  
GACGAGGGGCATCAAGCACAGAACATCAAGTGGAACCGGAAGGCCCTGCCAGCACTGCCAGATCA  
CTGAGGCCAGGTGGCTGAGAACCGCCCCGGGAGCCTCATCAAGCAAGGCCAAGCTCGACATT  
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCGATGGCATCCA  
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTGTCAACCGGCTGCATCAATGCCA  
CCCAGGGGGGAACCAAGGGGGAGTCCAGAACGCCAGAACAGCTCCACCAGCAGGTGCTCTGG  
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTGGAGAGGGCGCAGGACT  
TCGGGTACCAGTGCACCAAGCCAGTGCTCCTCTGCCTTGTGATCTGGCTATGGTAAAAT  
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCAGCAAATCCTGGCAAGTGACCCAGCT  
CTTCTCCCCAAACCCACGCGTGTCTGAAGGTGCCAGGAGCGCGATGCACTGCACTGCCAAA  
TGCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAAGATGGGGACTGTGGCTCT  
CCGTCACTCCATTCTCAGCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT  
GAGAAGAACACATCAGGCACTGCGCCACCTGCTTCACAGTACTTCCAACAACTTTAGAGGTAG  
GTGTATTCCCGTTTACAGATAAGGAAACTGAGGCCAGAGAGCTGAAGTACTGCACCCAGCAGC  
ACCAAGCTAGAAAGTGGCAGGCCAGGATTCAACCCCTGGCTGTCTAACCCCAAGGTTCTGCTCT  
GTCCAATTCCAGAGCTGTCTGGTACATTATGTCTCACAGGGACCCACATCCAAACATGTAT  
CTCTAAATGAAATTGTGAAAGCTCCATGTTAGAAATAATGAAAACACCTGA

## **FIGURE 146**

MRKHLSWWLATVCMLLFSHLSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK  
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNLHQQ  
VLWRLVQELCSLKHFCEFWLERGAGLRTMHQPVLLCLLAIWLMVK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 157-171

**N-glycosylation sites.**

amino acids 98-102, 110-114

**Tyrosine kinase phosphorylation site.**

amino acids 76-83

**N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

**Amidation site.**

amino acids 62-66

### **FIGURE 147**

GCCTTGGCCTCCAAAGGGCTGGGATTATAGCGTGACCAACCAGTCTGGTCCAGAGTCTCATTT  
CCTGATGATTTATAGACTCAAAGAAAACTCATGTTCAGAAGCTCTTCTCTTCTGGCCTCCTCT  
CTGTCTTCTTCCCTCTTCTTATTAAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG  
AAATCTTCATTTGCTTGTCACTGGGGTAGGTCACGTGAGTCTTAGTTTTATTTTGAAATT  
CAACTTCAGATTCAAGGGGTACATGTGAAGGTTGTTATGAGTATATTGCATGATGCTGAGG  
TTTGGGGT

## **FIGURE 148**

MFRSSLLFWPPLCLLSLFLLLILISSIYSESCKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE  
GLFYEYIA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-myristoylation site.**

amino acids 62-68

## **FIGURE 149**

GTCTCCGCGTCACAGGAACCTCAGCACCCACAGGGCGGACAGCGCTCCCTTACCTGGAGACTTGAC  
TCCC CGCGCCCCAACCCCTGTTATCCCTGACC GTCGAGGTGTCAGAGATCCTGCAGCCGCCAGTCC  
CGGCCCCCTCTCCGCCCCACACCCACCCCTGGCTCTTCTGTTTACTCCTCCCTTCATT CATA  
ACAAAAGCTACAGCTCCAGGAGCCAGCGCCGGCTGTGACCCAAGCCAGCGTGGAAAGAATGGGTT  
CCTCGGGACCGGCACGGATTCTGGATTCTGGTTAGTGTCCCATTCAAGCTTCCAAACCTGGAGGAA  
GCCAAGACAATCTCATATAATAGAGAATTAAGTGCAGAAAGACCTTGAATGAACAGATTGCTGAA  
GCAGAAGAAGACAAGATTAAGGAAACATATCCTCCAGAAAACAAGCCAGGT CAGAGCAACTATTCTT  
TGTTGATAACTGAAACCTGCTAAAGGCAATAACAGAAAAGGAAAAATTGAGAAAGAAAGACAATCTA  
TAAGAAGCTCCCCACTTGATAATAAGTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAAGT  
ATCGATGATTATGACTCTACTAAAGAGTGGATTGGATCATAAATTCAAGATGATCCAGATGGTCTCA  
TCAACTAGACGGGACTCCTTAACCGCTGAAGACATTGTCATAAAATCGTGC CAGGATTATGAAG  
AAAATGACAGAGCCGTGGT GACAAGATTGTTCTAAACTACTTAATCTCGGCCCTTATCACAGAAAGC  
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTACAAAAATTAACTCAAAGGAAGCCAACAA  
TTATGAGGAGGATCCAATAAGCCCACAAGCTGGACTGAGAATCAGGTGGAAAAATACCAGAGAAAG  
TGACTCCAATGGCAGCAATTCAAGATGGTCTGCTAAGGGAGAAAAGATGAAACAGTATCTAACACA  
TTAACCTTGACAAATGGCTGGAAAGGAGAACTAAAACCTACAGTGAAGACAAC TTGAGGAAC TCCA  
ATATTCCCAAATTCTATGCCCTACTGAAAAGTATTGATTGAGAAAAGAGCAAAGAGAAAGAAA  
CACTGATTACTATCATGAAAACACTGATTGACTTGTGAAGATGATGGTGAATATGGAACAATATCT  
CCAGAAGAAGGTGTTCTACCTGAAAAGTGGATGAAATGATTGCTCTCAGACCAAAACAAGCT  
AGAAAAAAATGCTACTGACAATATAAGCAAGCTTTCCAGCACC ATCAGAGAAGAGTCATGAAGAAA  
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAGGATTCCACAAA  
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAACAGAAGCCTATTGGAAGC  
CATCAGAAAAAAATTGAATGGTGAAGAAACATGACAAAAGGGAAATAAGAAGATTATGACCTT  
CAAAGATGAGAGACTTCATCAATAAACAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA  
GAAGCCGAGGCCATCAAGCGCATTAGCAGCCTGTAAAATGGCAAAGATCCAGGAGTCTTC  
CTGTTGAGAAAACATAATATAGCTAAACACTTCAATTCTGTGATTAAAATTTTGACCCAAGG  
GTTATTAGAAAGTGTGAATTACAGTAGTTAACCTTTACAAGTGGTAAAACATAGCTTCTCC  
GTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAA

## **FIGURE 150**

MGFLGTGTWILVLVLPIQAFPKPGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTPPENKPG  
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK  
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDFKIVSKLLNLGLITESQAHTLEDEVAE  
VLQKLISKEANNYEEDPNKPSTWTENQAGKIPFKVTPMAAIQDGFLAKGENDETVSNTLTLNGLE  
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV  
SYLENLDEMIALQTKNKLEKNATDNISKLFPAPEKSHEETDSTKEEAAKMEKEYGSLKDSTKDD  
NSNPGGKTDEPKGTEAYLEAIRKNIEWLKKHDKGKNGKEDYDLSKMRDFINKQADAYVEKGILDK  
EEAEAIKRIYSSL

**N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

**Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

**N-myristoylation sites:**

amino acids 143-148, 239-244

## **FIGURE 151**

CGGCTCGAGGCTCCGCCAGGAGAAAGAACATTCTGAGGGAGTCTACACCCGTGGAGCTCAA  
GATGGTCCTGAGTGGGGCCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGTTTATCTGC  
ATAATAACCAGCTCTAGCTGGAGGGCTGCATGCAGGGAAAGGTCAATTAAAGGTGAAGAGATCAGC  
GTGGTCCTCAATCGTGGCTGGATGCCAGCTGTCCCCCGTCATCTGGGTGTCCAGGGTCCAAG  
CCAGTGCCCTGTCACTGTGGGTGGGGCAGGGAGCCGACTCTAACACTACAGGCCAGTGAACATCATGG  
AGCTCTATCTGGTGCAGGAAATCCAAGAGACTTCACCTCTACCCGGGACATGGGGCTCAC  
TCCAGCTCGAGTCGGCTGCCTACCCGGGCTGGTCTGTGCACGGTGCCTGAAGCCGATCAGCC  
TGTCAAGACTCACCCAGCTCCCGAGAATGGTGGCTGGAAATGCCCATCACAGACTCTACTTCC  
AGCAGTGTGACTAGGGCAACGTGCCCGAGAACACTCCCAGGGCAGGCCAGCTGGGTGAGGGGT  
GAGTGGAGGAGACCCATGGCGGACAATCACTCTCTGCTCAGGACCCCCACGTCTGACTTAG  
TGGGCACCTGACCCTTGCTCTGGTCCCAGTTGGATAAAATTCTGAGATTGGAGCTCAGT  
CCACGGCTCCCCACTGGATGGTCTACTGCTGTGGAAACCTTGTAAAAACCATGTGGGTAAA  
CTGGGAATAACATGAAAAAGATTCTGTGGGGTGGGGGGAGTGGTGGGAATCATCTGCT  
TAATGGTAACTGACAAGTGTACCCCTGAGCCCCGAGGCCAACCCATCCCCAGTTGAGCCTTATA  
GGGTCAAGTAGCTCCACATGAAGTCTGTCACTCACCCTGTGCAAGGAGAGGGAGGTGGTCTATA  
GAGTCAGGGATCTATGGCCCTGGCCAGGCCAACCCCTTCCCTTAATCCTGCCACTGTCTATA  
TGCTACCTTCTATCTCTCCCTCATCATCTTGTGGCATGAGGAGGTGGTGTAGAA  
GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTAAAAACCAA  
GATACAATCAAATCCCAGATGCTGGTCTCATCTCCATGAAAAAGTGTCTGACATATTGAGA  
AGACCTACTTACAAGTGGCATATAATTGCAATTATTATAATTAAAGATAACCTATTATATT  
TCTTTATAGAAAAAGTCTGGAAGAGTTACTTCATTGTAGCAATGTCAGGGTGGTGGCAGTAT  
AGGTGATTTCTTTAATTCTGTTAATTATCTGTATTCCTAATTTTCTACAATGAAGATGA  
ATTCCCTGTATAAAAATAAGAAAAAGAAATTATCTTGAGGTAAGCAGAGCAGACATCATCTGA  
TTGTCCTCAGCCTCCACTTCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTCTGGTTGG  
TTGTAGTAGTGTAGCAGGAAACAGATCTCAGCAAGCCACTGAGGAGGGCTGTGAGTTTGT  
GTGGCTGGATCTCTGGTAAGGAACCTAAAGAACAAAAATCATCTGTAATTCTTCTAGAAG  
GATCACAGCCCCCTGGGATCTCAAGGATTGGGATCCAGCTCTAAGAAGGCTGCTGTACTGGTGA  
ATTGTGCCCCCTCAAATTCACATCTTCTTGGAAATCTCAGTCTGTGAGTTATTGGAGATAAG  
GTCTCTGAGATGTAGTTAGACAAGGTATGCTGGATGAAGGTAGACCTAAATTCAATAT  
GACTGGTTCTGTATGAAAGGAGAGGACACAGAGACAGAGGAGACGCCAGGGAAAGACTATGTA  
AAGATGAAGGACAGAGATCGGAGTTTGCAGCCACAAGCTAAGAACACCAAGGATTGTGGCAACC  
ATCAGAAGCTGGAGAGGCAAAAGAAGAATTCTTCCCTAGAGGTTAGAGGGATAACGGCTCTG  
CTGAAACCTTAATCTCAGACTTCCAGCCTCTGAACGAAGAACAGATAAAATTTCGGCTGTTTAA  
GCCACCAAGGATAATTGGTTACAGCAGCTAGGAAACTAATACAGCTGCTAAATGATCCCTGT  
CTCCTCGTGTAACTCTGTGTGCTGCTCTCCACATGACCAAGTGTCTTGTGACCAA  
TAGAATATGGCAGAAGTGTGGCATGCCACTTCAAGATTAGTTAAAGACACTGCAGCTTC  
TACCTGAGCCCTCTCTGCAAGGCCACCCACGGCCCCAATCTATCTGGCTCACTCGCTCTGGGG  
AAGCTAGCTGCCATGCTATGAGCAGGCTATAAAGAGACTTAGCTGGTAAAAAATGAAGTCTCCT  
GCCACAGCCACATTAAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATGATTTGTGTTT  
AAGTTGCTCAGTTGGCTAACCTGTATGCAAGCAATAGATAAATAATGCAAGAACAGAG

## **FIGURE 152**

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESVVPNRWLDASLSPVILGVQGGS  
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP  
VRLTQLPENGGWNAPITDFYFQQCD

**N-myristoylation sites.**

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

**Interleukin-1 signature.**

amino acids 111-131

**Interleukin-1 proteins.**

amino acids 8-29, 83-120, 95-134, 64-103

### **FIGURE 153**

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC  
CCTGCAGAAATCTGTGAGCTTTCTTATGGGGACCCCTGGCCACCAAGCTGCCTCCTTCTCTTG  
CCCTCTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCCTGCAGGCTTGACAAGTCCAAC  
TTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA  
CAACACAGACGTTCGTCTCATTGGGGAGAAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT  
ATCTGATGAAGCAGGTGCTGAACCTCACCCCTGAAGAACTGCTGTTCCCTCAATCTGATAGGTTC  
CAGCCTTATATGCAGGAGGTGGTGCCTTCTGGCAGGCTCAGAACAGGCTAACGCACATGTCA  
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAGCTGAAGGACACAGTGAAAAAGC  
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTGCTGTTATGTCTCTGAGAAAT  
GCCTGCATTTGACCAAGAGCAAAGCTGAAAATGAATAACTAACCCCCCTTCCCTGCTAGAAATAA  
CAATTAGATGCCCAAAGCGATTTTTAAACAAAAGGAAGATGGGAAGCCAAACTCCATCATG  
ATGGGTGGATTCCAAATGAACCCCTGCCTAGTTACAAAGGAAACCAATGCCACTTTGTTATA  
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTATTGATAACATTGTAACTGGTGTTC  
TATACACAGAAAACAATTATTAAATAATTGTCTTTCCATAAAAAGATTACTTCCAT  
TCCTTAGGGAAAAAAACCCCTAAATAGCTCATGTTCCATAATCAGTACTTTATATTATAAA  
TGTATTATTATTATAAGACTGCATTTATTATCATTATTATAATATGGATTATT  
AGAAACATCATTGCTACTTGAGTGTAAAGGCTAATTGATATTATGACAATAATT  
AGAGCTATAACATGTTATTGACCTCAATAAACACTGGATATCCC

## **FIGURE 154**

MAALQKVSSFLMGTIATSCLLLALLVQGGAAAPISSHCRLDKSNFOOPYITNRTFMLAKEASL  
ADNNNTDVRЛИGEKLFHGVSMERCYLMQVLNFTLEEVLFQPSDRFQPYMQEVVPFLARLSNRSL  
TCHIEGDDLHIQQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 54-58, 68-72, 97-101

**N-myristoylation sites.**

amino acids 14-20, 82-88

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 10-21

## **FIGURE 155**

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT  
CAGTCAGTGCCCGACTTGTGACTGAGTGTGCAGTGCCCAGCATGTACCAGGTCACTGCAGAGGGC  
TGCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC  
TGCCAGGTTGGGCTGGGGCCAAGTGGAGTGGAGAAACTGGGATCCCAGGGGAGGGTGCAGAT  
GAGGGAGCAGCCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTCTACAGGTGGTTGCAT  
TCTTGGCAATGGTCATGGAACCCACACCTACAGCCACTGGCCAGCTGCTGCCAGCAAAGGG  
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCCTAGAGCCTGCTAG  
GCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTAACAGCAGGGCCATCT  
CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGACCTGTACCACGCCGT  
TGCCTGTGCCCGCACTGCGTCAGCCTACAGACAGGCTCCACATGGACCCCCGGGCAACTCGGA  
GCTGCTCTACCACAACCAGACTGTCTTACAGGCGGCCATGCCATGGCGAGAAGGGCACCCACA  
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTAGCTGTGTGTGCAGGGCCCGT  
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTGGAAACCTGGAGCCAGGTGTACA  
ACCACTGCCATGAAGGGCCAGGATGCCAGATGCTTGGCCCTGTGAAGTGTCTGGAGCAG  
CAGGATCCCGGACAGGATGGGGGCTTGGGAAACCTGCACTCTGCACATTGAAAGGTTTCAA  
CAGCTGCTGCTTAGGGCCGGGAAGCTGGTGTCTGTCACTTCTCTCAGGAAAGGTTTCAA  
GTTCTGCCATTCTGGAGGCCACCACTCTGTCTTCCCTTCCATCCCTGCTACCCCTG  
GCCCACAGGCACCTCTAGATAATTCCCTTGCTGGAGAAGAAAGGCCCTGGTTTATT  
TGTTGTTTACTCATCACTCAGTGAGCATCTACTTGGTGCATTCTAGTGTAGTTACTAGTCTT  
TTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATAGAGATTATCAAATAAATAT  
CTTTATTAATGAAAAAA

## **FIGURE 156**

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHTYSHWPSCCP SKGQDTSEELL RWSTVPVPPLEPA  
RPNRHPE SCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS  
ELLYHNQTVFYRRPCHGEKGTHKGYCLERRLYRVSLACVCVR PRVMG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-32

**N-glycosylation site.**

amino acids 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 127-135

**N-myristoylation sites.**

amino acids 44-50, 150-156

## **FIGURE 157**

CCGGCGATGTCGCTCGTGCAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC  
GACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC  
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTGCAACAGGGACTATTCA  
ATTTTGATGAATGTAAGCTGGGTACTCCGGCAGATGCCAGCATCCGCTTGTGAAGGCCACCAA  
GATTTGTGTGACGGCAAAAGCAACTTCCAGTGTGAGGTGCAATTACACAGAGG  
CCTTCCAGACTCAGACCAGACCCCTCTGGTGGTAAATGGACATTTCCATACATCGGCTTCCCTGTA  
GAGCTGAACACAGTCTATTCATTGGGCCATAATATCCTAATGCAAATATGAATGAAGATGG  
CCCTTCCATGTCTGTGAATTTCACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAAA  
AGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAAACATCACTGCTTGTAAAGAAGAATGAGGAGACA  
GTAGAAGTGAACCTCACAAACACTCCCTGGGAAACAGATACTGGCTTATCCAACACAGCAC  
TATCATCGGGTTTCTCAGGTGTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA  
TTCCAGTGACTGGGATAGTGAAGGTGCTACGGTGCAGTGACTCCATATTCCTACTTGTGGC  
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCACAAAACAGCGTCCCTTCCCTCT  
GGATAACAAACAAAGCAAGCCGGAGGCTGGCTGCCTCTCCTCTGCTCTGCTGGTGGCCA  
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTT  
TCTACCACCAACTACTGCCCTTCAATTAGGTTCTTGTGGTTACCCATCTGAAATATGTTCCA  
TCACACAATTTGTTACTTCAGTGAATTCTCAAACCAATTGCGAGAAGTGAGGTCACTCCTGAA  
AGTGGCAGAAAAGAAAATAGCAGAGATGGTCCAGTGCAGTGGCTGCCACTCAAAGAAGGCA  
GCAGACAAAGTCGCTTCCCTTCCAATGACGTCAACAGTGTGCGATGGTACCTGTGGCAA  
GAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTTCCCCCTGCCCTAACCTTCTGCA  
GTGATCTAAGAAGCCAGATTCTGCACAAATACGTGGTGGCTACTTAGAGAGATTGATACA  
AAAGACGATTACAATGCTCTCAGTGTGCCCAAGTACCACTCATGAAGGATGCCACTGCTTT  
CTGTGCAGAACCTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAGATCACAAGCCTGCCACG  
ATGGCTGCTGCCCTTGTAG

## **FIGURE 158**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGDLRDLRVEPVTTSVATGDYSILMNWSW  
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP  
NANMNEEDGPSMSVNFTSPGC LDHIMKYKKCVKAGSLWDPNITACKNEETVEVNFTTPLGNRYMALIQH  
STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPTGVPFPLDNNK  
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTLLPPIKVLVVYPSEICFHHTICYFTEFL  
QNHCRCSEVILEKWQKKIAEMGPVQWLATQKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA  
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVCPKYHLMKDÀTAFCAELLHVVKQQVSAGKRSQACHD  
GCCSL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**Transmembrane domain:**

amino acids 290-309

**N-glycosylation sites.**

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283  
- 287

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

**Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

**N-myristoylation site.**

amino acids 116-122

**Amidation site.**

amino acids 488-492

## **FIGURE 159**

AGCCACCAGCGAACATGACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT  
GTCGATATTGGGGCTTGCCTTCTGAGTGAGGCGGCAGCTCGGAAATCCCCAAGTAGGACATA  
CTTTTTCCAAAAGCCTGAGAGTTGCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC  
ATCATCAATGAAAACCAGCGCTTCCATGTCACGTAACATCGAGAGCCGCTCACCTCCCCCTG  
GAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCAGTGTAGGA  
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCATCCAGCAA  
GAGACCCCTGGTCGTCGGAGGAAGCACCAAGGCTGCTCTGTTCTTCCAGTTGGAGAAGGTGCT  
GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCACTCCACCATGTGCAGTAAGAGGTGCATATCC  
ACTCAGCTGAAGAAG

## **FIGURE 16O**

MTVKTLHGPAMVKYLLSILGLAFLSEAAARKIPKVGHFFQKPESCPPVPGGSMKLDIGIINEN  
QRVSMSRNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRLGCINAQGKEDISMNSVPQQETLVV  
RRKHQGCSVSFQLEKVLVTVGCTCVTPVIHHVQ

**Signal sequence:**

amino acids 1-30

**N-glycosylation site.**

amino acids 83-87

**N-myristoylation sites.**

amino acids 106-111, 136-141

## **FIGURE 161**

ACACTGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGTCAGGACTCCCAGG  
ACAGAGAGTGCACAAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGGATTC  
CAGCCCCCTGCCACCCACAGACACAGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGCAGCAC  
AGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCCTGTGCCCTGGTCTGCTGTCC  
TGGCACTGGGCAGGCCAGTGGCTTTCTCTGGAGAGGCTTGTTGGGGCCTCAGGACGCTACC  
CACTGCTCTCCGGGCTCTCCGCGCTCTGGACAGTGACATACTCTGCCTCCCTGGGACAT  
CGTCCTGCTCCGGCCCCGTGCTGGCGCTACGCACCTGCAGACAGAGCTGGTGTGAGGTGCC  
AGAAGGAGACCGACTGTGACCTCTGCTCGCTGTGGCTGCACTTGGCGTGCATGGGACTGG  
GAAGAGCCTGAAGATGAGGAAAAGTTGGAGGAGCAGCTGACTCAGGGTGGAGGAGCCTAGGAA  
TGCCTCTCCAGGCCAAGTCGTCTCTCCAGGCCAACCTACTGCCGCTGCGCTCTGC  
TGGAGGTGCAAGTGCCTGCTGCCCTTGTCAGTTGGTCAGTCTGTTGGCTCTGTGGTATATGAC  
TGCTTCGAGGCTGCCCTAGGGAGTGAAGTACGAATCTGGCTCTATACTCAGGCCAGGTACGAGAA  
GGAACATCAACCACACACAGCAGCTGCCCTGCCCTGGCTAACAGTGTCAAGCATGGTACA  
ACGTGCATCTGGTTCTGAATGTCCTGAGGAGCAGCATTGCCCTCTCCCTGTA<sup>CTGG</sup>AATCAG  
GTCCAGGGCCCCCAAAACCCGGTGGCACAAAACCTGACTGGACCGCAGATCATTACCTTGA  
CCACACAGACCTGGTTCTGCTCTGTATTCAAGGTGTTGGCTCTGGAAACCTGACTCCGTTAGGA  
CGAACATCTGCCCTCTGGAGGACCCCGCAGCACCCAGAACCTGGCAAGGCCGCGACTG  
CGACTGCTGCCCTGCAGAGCTGGCTGCTGGACGCACCGTGTGCTGCCCGCAGAACCGGACT  
GTGCTGGCGGGCTCCGGGTGGGACCCCTGCCAGCCACTGGTCCACCGCTTCTGGAGAACG  
TCACTGTGGACAAGTTCTCGAGTTCCATTGCTGAAGGCCACCCCTAACCTCTGTTCAAGGTG  
AACAGCTGGAGAACGCTGCAGCTGCAGGAGTGTTGTGGCTGACTCCCTGGGCCCTCTCAAAGA  
CGATGTGCTACTGTGGAGACACGAGGCCAGGACAACAGATCCCTGTGCCCTGGAAACCCA  
GTGGTGTACTTCACTACCCAGAAAGCCTCACGGAGGGCAGCTGCCCTGGAGAGTACTTACTA  
CAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGGCCATGGGCTG  
CCCCATGGACAAATACATCCACAAGCGCTGGGCCCTGCTGTGGCTGCCCTACTCTTGCCTG  
CTGCGCTTCCCTCATCTCTCTCAAAAGGATCACCGAACAGGGTGGCTGAGGCTCTGAA  
CAGGACGTCCGCTCGGGGGCGGGCGCCAGGGGCCGCGCGCTCTGCTCTACTCAGCCGATGA  
CTCGGGTTCTGAGGCCCTGGGGCGCCCTGGCGTGGCCAGTGGCGCTGCGCTGCGCGTGG  
CCGTAGACCTGTGGAGGCCGTGTAACGTGAGCGCGCAGGGGCCGCTGGCTTGGTTCA CGCGCAG  
CGCGCCAGACCTGCAAGGAGGGCGCGTGGTGGCTTGTCTTCTCCTGGCTGCGCGTGGCGT  
GTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCGGGCGCACGGCCCGCACGACGCCCTCC  
GCGCCTCGCTCAGCTGCGTGTGCCGACTCTTGCAAGGGCCGGCGCCGGCAGCTACGTGGGG  
GCCCTGCTCGACAGGCTGCTCCACCCGGACGCCGTACCCGCCCTTCCGCACCGTGCCGTCTT  
CACACTGCCCTCCCAACTGCCAGACTCTGGGGCCCTGCAAGCAGCCCTGGATAGCTACTTC  
GGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTCAGCAAGCCCTGGATAGCTACTTC  
CATCCCCGGGACTCCCGCGCCGGACGCCGGTGGGACCAAGGGCGGGACCTGGGGCGGGGA  
CGGGACTAAATAAAGGCAGACGCTGTTTCTAAAAAA

## **FIGURE 162**

MPVPWFLLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRILWDSIDLCLPGDIVPAPGPVLAPTHLQTELVL  
LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSFOAYPTARCVILLEV  
QVPAALVQFGQSVGSVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNVS  
EEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQN  
LWQAARLRLTLQSWLLDAPCSLPAEAALCWWRAPGGDPQCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ  
VNSSEKLQLQECLWADSLGPLKDDVLLLETTRGPQDNRSILCALEPSGCTSLPSKASTRAARLGEYLLQDLQS  
GQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLLLLKKDHAKGWLRLLKQDVRSGAAARG  
RAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRRTQLQEGGVVVLLFSP  
GAVALCSEWLQDGVSAGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTPVVF  
LPSQLPDFL GALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

**Signal sequence:**

amino acids 1-20

**Transmembrane domain.**

amino acids 453-475

**N-glycosylation sites.**

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,  
334-337, 357-360, 391-394

**Glycosaminoglycan attachment site.**

amino acids 583-586

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 552-555

**N-myristoylation sites.**

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,  
692-697, 696-701, 700-705

## **FIGURE 163**

GGGAGGGCTCTGTGCCAGCCCCATGAGGACGCTGCTGACCACATTGACTGTGGGATCCCTGGCT  
GCTCACGCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCCAGTCCAGCAACTTGA  
AAACATCCTGACGTGGGACAGCGGGCAGAGGGCACCCAGACACCGTCTACAGCATCGAGTATA  
AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTCAAGCAGATCACCCGAAGTCTGC  
AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTACCGCT  
GTCAGTGCAGGGAGGGCCGGTCAGCCACCAAGATGACTGACAGGTTAGCTCTGCAGCACACTAC  
CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGGAGATCGATTAGCTAGATGATTTGTTCATCTTA  
CCCCCACGCCAATCCGTGCAGGGCATGGCACCCGGCTAACCTGGAAAGACATCTCCATGACCTG  
TTCTTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGAGGGAAAGCAGAGAGA  
ATATGAGTTCTCGGCCTGACACAGACTTCCCTGGCACCATCATGATTGGGTTCCCA  
CCTGGCCAAGGAGGTGCCCCCTACATGTGCCAGTGAAGACACTGCCAGACCCGACATGGACC  
TACTCCCTCTCGGAGCCTTCCATGGGCTTCCATGCCAGTACTCTGCTACCTGAG  
CTACAGATATGTCACCAAGGCCGCTGCACCTCCAACTGGCTAACGTCAGGGAGTCTGACTT  
TCCAGCGCTGCCCTCATCCAGGAGCACGCTCTGATCCCTGCTTGTACCTCAGGGGGCCAGGAGC  
AGTCTGGCCAGGCTGTCCAGTACTCCAGATCAGGGTGTCTGGACCCAGGGAGCCCGCAGGAGC  
TCCACAGGGCATAGCCTGTCCAGATCACCTACTTAGGGCAGCCAGACATCTCATCCTCCAGC  
CCTCCAAAGTGCACCCCTCCCAAGTCTCTCCACTGCTCATGCCCAAACGCTGCCCTGAG  
GTCGGGGCCCATCTATGACCTCAGGTGACCCCGAAGCTCAATTCCATTACGCCACA  
GGCCATCTAAGGTCAGCCTCCATGCCCTCAAGGACTCCAGTGGGACACTTTCTAGTCTAAA  
CCTATGGGTATGCATGGAAGGTTCTGGCAAGAGACTCCCCACTGGGACACTTTCTAGTCTAAA  
CACCTTAGGCCTAAAGGTCAAGCTCAGAAAGGCCACAGCTGAAAGCTGATGTTAGGTGGCCT  
TTCTCTGCAAGGAGGTGACCTCTGGCTATGGAGGAATCCAAGAAGCAAATATTGCAACAGC  
CCCTGGGATTGACAGACAGAACATCTGACCCAAATGTGCTACACAGTGGGAGGAAGGGACA  
CCACAGTACCTAAAGGCCAGCTCCCCCTCCTCTCAGTCAGATCGAGGGCCACCCATGTC  
CCTCCCTTGCAACTCTCCCTCCGGTCCATGTTCCCTCGGACCAAGGTCCAAGTCCCTGGGCC  
TGCTGGAGTCCCTTGTGTCCAGGATGAAAGCCAAGAGCCCAGCCCTGAGACCTCAGACCTG  
GAGCAGGCCACAGAACTGGATTCTCTTCAAGGGCTGGCCCTGACTGTGCAGTGGAGTCTG  
AAGGGAAATGGGAAAGGCTGGTGTCTCCCTGTCCCTACCCAGTGTCACTCCTGGCTGTCA  
ATCCCATGCTGCCATGCCACACACTCTGCGATCTGCCCTCAGACGGGTGCCCTGAGAGAAGC  
AGAGGGAGTGGCATGCAGGGCCCTGCCATGGGTGCGCTCTCACCGGAACAAAGCAGCATGATA  
AGGACTGCAGCGGGGAGCTGGGAGCAGCTGTGAGACAAGCGCTGCTGAGCCCTG  
CAAGGCAGAAATGACAGTGAAGGAGGAATGCAAGGGAAACTCCGAGGTCCAGAGCCCCACCTC  
CTAACACCATGGATTCAAAGTGTCAAGGAAATTGCTCTCCCTGCCCATTCTGGCCAGTTTC  
ACAATCTAGCTGCAGAGACATGAGGCCCTGCCTTCTGTCAATTGTTCAAAGGTGGGAAGAGA  
GCCCTGGAAAAGAACCAAGGCCCTGGAAAAGAACCAAGAGAAGGAGGTGGCAGAACAGAACACTGC  
ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGCCCTGAGCTCA  
TTCCCAAGGCCACTGCCTGACGTTGACGATTTCAGCTTCTGCTATTGTTCAAAGGTGGGAAGAGA  
GAAATGCAGGTCCACCAGGGAGGGAGACACACAAGCCTTTCTGCAGGCAGGAGGTTCA  
ATCCTGAGAATGGGTTTGAAGGAAGGTGAGGGCTGTGGCCCTGGAGGGTACAATAACACAC  
TGTACTGATGTCAACACTTGCAGCTGCTGGGCTGAGCCCTGAGGGCTCAAATTCCAGC  
CTCACCAACTCACAAGCTGTGTCACTTCAAACAAATGAAATCAGTGCCAGAACCTCGGTTCTC  
ATCTGTAATGTGGGATCATAACACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAGTCATG  
TCTTTAAAGTGTCTAAATAGTGCCTGGTACATGGCAGTGCCAATAACGGTAGCTATTTAAAAA  
AAAAAAAA

## **FIGURE 164**

MRTLLTILTGVSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW  
VAKKGCCRITRKSCNLTVEGNLTELYYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVCIS  
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMHLGGKOREYEFFGLTPDT  
EFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFSGAFLFSMGFLVAVLCYLSYRYVTKPPAP  
PNSLNQQRVLTFQPLRFIQEHVLIPIPVDLSPGSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT  
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFPFYAPQAISKVQPSY  
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPKGQLQKEPPAGSCMLGGSLQEVTSIAM  
EESQEAKSLHQPLGICTDRTSDPNVLHSGEEGTPQYLKGQLPLLSSVQIEGHPMMSLPLQPPSGPC  
SPSDQGPSPWGLLESLVCPKDEAKSPAPETSDLEQPTELDSLFRGLALTQWES

**Signal sequence.**

amino acids 1-17

**Transmembrane domain.**

amino acids 233-250

**N-glycosylation sites.**

amino acids 80-83, 87-90, 172-175

**N-myristylation sites.**

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

## **FIGURE 165**

TGGCCTACTGGAAAAAAAAAAAAAAGTCACCCGGGCCCCGGTGGCCACAACATGG  
CTGCGGCCGGGCTGCTCTCTGGCTGTCGTGGCTGGGGCGCTCTGGTGGTCCCAG  
TCGGATCTCAGCCACGGACGGCGTTCTCGGACCTCAAAGTGTGCAGGGACGAAGAGTCAGCAT  
GTTAACGTACCGTGGAAAGCTCTGAAGACTTCACGGCCCTGATTGTCTGTTGTGAATTAA  
AAAAAGGTGACGATGTATATGTCTACTACAAACTGGCAGGGGATCCCTGAACTTGGCTGGA  
AGTGTGAACACAGTTGGATATTTCAAAAGATTGATCAAGGTACTTCATAAAACACGGA  
AGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCTGCTTGAGGAGGAAGAGATGATT  
TTAATAGTTATAATGTAGAAGAGCTTTAGGATCTTGGAACTGGAGGACTCTGTACCTGAAGAG  
TCGAAGAAAGCTGAAGAAGTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGCGTGA  
ACTTGACCCCTGTGCCTGAGCCCGAGGCATTAGCAGACTGATTAGGAGATGGAGAAGGTGTTCT  
CAGAGAGCACCGAGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCCTCACACCAGCGGT  
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTCGTTGGACACTTTGAAGAAATTCTGCACGATAA  
ATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA  
AGACAGATGCTTACAAAGCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCCTTATT  
CATTACAGCAAAGGATTCGTTGGCATCAAAATCTAAGTTGTTTACAAAGATTGTTTTTAGTA  
CTAAGCTGCCTGGCAGTTGCATTTGAGCCAACAAAAATATATTATTTCCCTCTAAGTA  
AAAAAAAAAAAAA

## **FIGURE 166**

MAAAPGILLFWLFVLGALWWVPGQSDLSHGRRFSDLKVC~~GDEEC~~SMLMYRGKALEDFTGPDCRFVN  
FKKGDDVVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHIPADETDFVC~~FEGGRD~~  
DFNSYNVEELLGSLELEDSPPEESKKAEEVSQHREKSPPEESRGRELDPVPEPEAFRADSEDGE~~G~~GA  
FSESTEGLQGQPSAQESHPHTSGPAANAQGVQSSLDTFEEILHDKLKVPGSESRTGNSSPASVER  
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYKDCF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 294-298

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34

**Tyrosine kinase phosphorylation site.**

amino acids 67-76

**N-myristoylation sites.**

amino acids 205-211, 225-231, 277-283

**Amidation site.**

amino acids 28-32

## **FIGURE 167**

## **FIGURE 168**

MSRVVSLLLGAALLCGHGFCCR VVSGQKVC FADF KHP CYK MAYF H E LSS RVS F QEARL ACESE  
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDFWIGLWRNGDQTS GACP DLYQWS DGSNSQ  
YRNWYTDEPSCGSEKCVV MYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAPVEK  
PYLTNQPGDTHQN VVVTEAGIIPNLIYVVIPTIPLL LILVAFGTCCFQMLHKS KGR TKTSPNQ  
STLWISKSTRKESGM EV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89, 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145, 212-217